

Figure 1

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Figure 6. The effect of the number of iterations (n) on the accuracy of the proposed algorithm. The figure shows two plots side-by-side. The left plot shows the error norm $\|e\|_2$ versus n , ranging from 0 to 100. The right plot shows the relative error $\frac{\|e\|_2}{\|x\|_2}$ versus n , ranging from 0 to 100. Both plots show a decreasing trend as n increases, indicating convergence.

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Figure 2

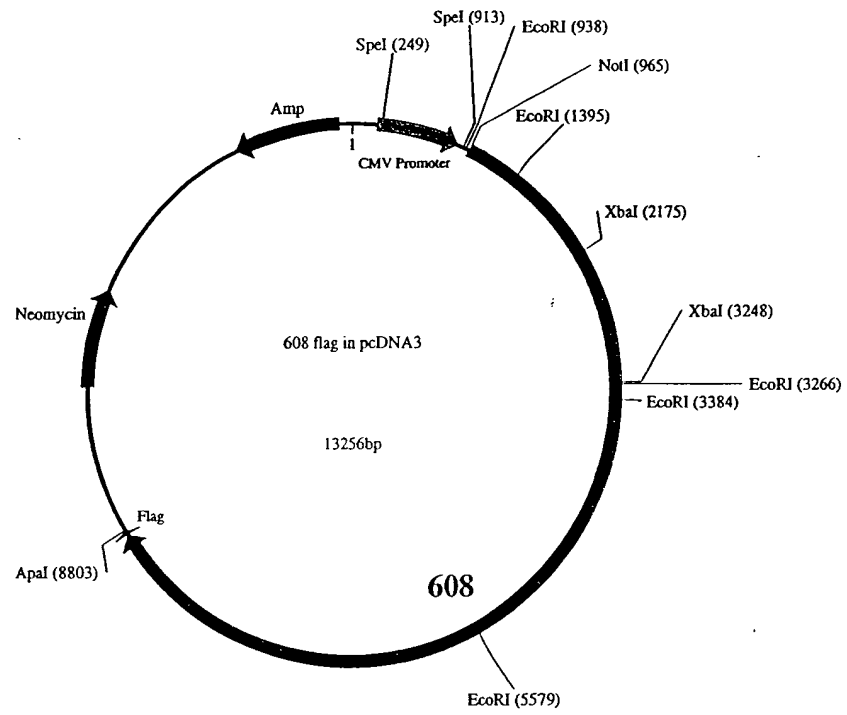


Figure 3

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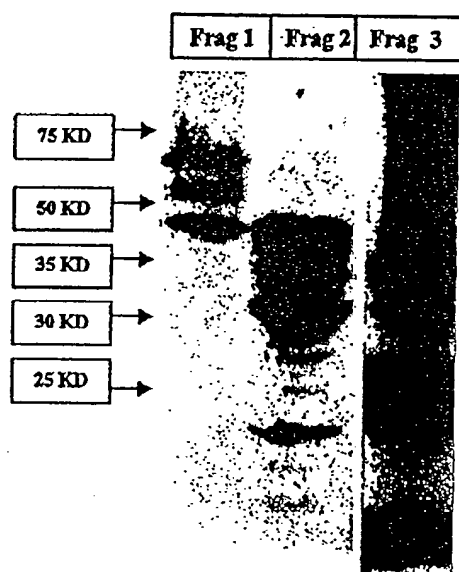
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Figure 4



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Figure 5

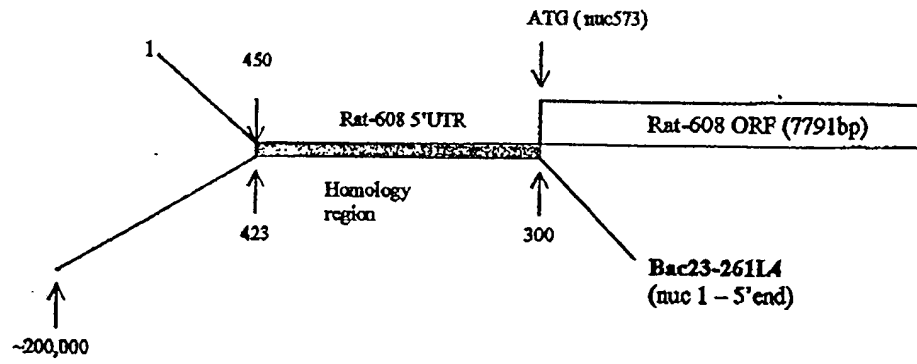
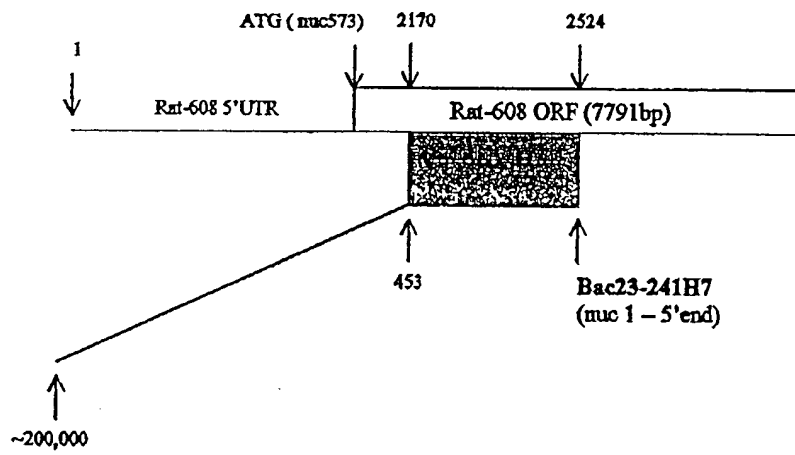


Figure 6



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Figure 7

Nuc 1

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↓ Nuc 390

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Exon 4 ? (Nuc 11286) ↓

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Nuc 11680 ↑

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Nuc 11967 ↑

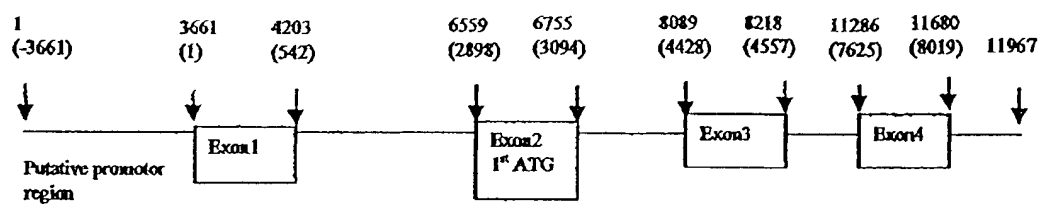
(SEQ ID NO:3)

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Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9



[illegible]

cDNA_rat genomic_hu	1	1	ogagagacgacagaaggttacggctgcgagaagacgacagaaggggtccag
cDNA_rat genomic_hu	51	1	aaaaaggaaagtgcctggaggggagtggggacaaaagcagacgaagtga
cDNA_rat genomic_hu	101	1	atgtcacttcagtgaactgagggccaggcaaaaagcgcggaaggattttgt
cDNA_rat genomic_hu	151	1	gtagccttgggaocctttcatagacactgatgacacgtttacgaaaaatag
cDNA_rat genomic_hu	201	1	aaattttgaggagaaaagcctggggccttcggaaaggagtgattgattagta
cDNA_rat genomic_hu	251	1	cttgcaagtttagtgactttaaggagaactaactaatgtatactattga
cDNA_rat genomic_hu	301	1	gggaggaggagagagcattacagagtttcagcagcagcaggaaagccttg
cDNA_rat genomic_hu	351	1	gttaatttggaaatggatgatagcattaaataacagaagcgctccagg
cDNA_rat genomic_hu	401	1	tctctgaagottoagctcccccagotgaagccagaaaagactaagccaac
cDNA_rat genomic_hu	451	1	taagccttttgatcccttgggaagcaagaactttccttcctcggggtga
cDNA_rat genomic_hu	501	1	agactctcctcagaagatttcctgtctctgcctatgttacaaggagaaac
cDNA_rat genomic_hu	551	1	aaaaccaagacagaagagctcaggatgcagggtgagaggcagggaagtcag
cDNA_rat genomic_hu	601	1	oggttggtgtgatctccctcaactgctgtctgcctgggtggtcaacccctggga
cDNA_rat genomic_hu	651	1	gcagggcctgtcctgcgcgctgtgcctgctatgtgccacagaggtgcac
cDNA_rat genomic_hu	701	1	tgtacatttcggtaacctgaacctccatcccagatgggaatcccgccaatgt
cDNA_rat genomic_hu	751	1	ggaacgaataaatttaggatataacagccttactagattgacagaaaacg
cDNA_rat genomic_hu	801	1	actttgatggcctgagcaaaactggagttactcatgotgcaagtaatggc
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cDNA_rat genomic_hu	901	1	cttaaaaatgagctatacaaaagtcacaaatcattcggaaggatactttct

cDNA_rat	951	acggactcgggagcttggtccgggtgcacctggatcacacaacattgaa
genomic_hu	1	-----
cDNA_rat	1001	ttcatcaacctgaggccttttatggacttacctogctccgcttggtaca
genomic_hu	1	-----
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genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	1201	aaacotagaaagcctgtatttgcattgaaacccatggacctgtgactgcc
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genomic_hu	1	-----
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genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	1651	cacaaatottgtgtgcagtgtagattataatcacatccagccagtggtgc
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genomic_hu	1	-----
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genomic_hu	1	-----
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cDNA_rat	2051	attgccotgagctgtccagggaaggagaccccttcacctcacttggatg
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genomic_hu	1	-----
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20/90

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genomic_hu	1	-----		
cDNA_rat	5551	ttcatcagganttgaaatatccaagggacacagaaaagccggttccacg		
genomic_hu	1	-----		
cDNA_rat	5601	tgcttcccaatggcaccttgctccatccagagggtcagtattcaggaccgt		
genomic_hu	1	-----		
cDNA_rat	5651	ggacagtacctgtgctctgcatttaataccactggcgtagaccattttca		
genomic_hu	1	-----		
cDNA_rat	5701	tgtotctttgtctgtggtttttacccggcaaggattttggacagacatg		
genomic_hu	1	-----		
cDNA_rat	5751	tcaaggagaccacagttcactttggaagtactgtggaactaaagtgcaga		
genomic_hu	1	-----		
cDNA_rat	5801	gtggagggtatgccgaggcctacggtttctctggatacttgcaaaccaaac		
genomic_hu	1	-----		
cDNA_rat	5851	ggtgggtctcagaaaacggccaagggaagcagaaagggtctgggtaacacctg		
genomic_hu	1	-----		
cDNA_rat	5901	atggaacattgatcatotataatctgagtcctttatgatcgtgggttttac		
genomic_hu	1	-----		
cDNA_rat	5951	aagtgtgtggccagcaacccatctggccaggattcactgttggttaagat		
genomic_hu	1	-----		
cDNA_rat	6001	acaagtcatcacagctccccctgtcattatagagcaaaagaggcaagcca		
genomic_hu	1	-----		
cDNA_rat	6051	tcgttgggggttttaggtggaagtttgaaaactgcctgcactgcaaaagga		
genomic_hu	1	-----		
cDNA_rat	6101	actccccagcctagtgttcactgggtcctttatgatgggactgaactaaa		
genomic_hu	1	-----		
cDNA_rat	6151	accattgcagttgactcattccagattttcttgatatccaaatggaactc		
genomic_hu	1	-----		
cDNA_rat	6201	tgtatataagaagcatogctccttcagtgaggggcacttatgagtgcat		
genomic_hu	1	-----		
cDNA_rat	6251	gccaccagctcctcaggctcagagagaagggtagtgattcttactgtgga		
genomic_hu	1	-----		

00005430 : 042202

cDNA_rat 6301 agagggagagacaatccccaggatagaaactgcctctcagaaatggactg
 genomic_hu 1 -----
 cDNA_rat 6351 aggtgaatttgggtgagaaattactactgaactgctcagctactgggat
 genomic_hu 1 -----
 cDNA_rat 6401 ccaaagcctagaataatctggaggctgccatccaaggctgtcatogacca
 genomic_hu 1 -----
 cDNA_rat 6451 gtggcacagaatGGGCAGCCGAATCCACGTCTACCCAAATGGATCCTTg
 genomic_hu 1 -----TGGGCAGCTGGATCCACGTCTACCCTAATGGATCCCTGt
 cDNA_rat 6501 tggttgggTCAGTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCA
 genomic_hu 40 ttatttgaTCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCA
 cDNA_rat 6551 AGAAACAAATGGGAGATGACCTAGTCCTGATGCATGTccgcctgAGATT
 genomic_hu 90 AGAAACAAATGGGGATGATCTGATACTGATGCATGTtagcctaAGACT
 cDNA_rat 6601 GACACCTGCCAAATTGAACAGAAGCAGTATTTTAagAAGCAAGTGCTCC
 genomic_hu 140 GAAACCTGCCAAATTGACCACAAGCAGTATTTTAgaAAGCAAGTGCTCC
 cDNA_rat 6651 ATGGGAAGATTTCCAAGTTGACTGCAaggcctotGGCTCCCCGTGTCCT
 genomic_hu 190 ATGGGAAGATTTCCAAGTAGATTGCAaagcttccGGCTCCCCAGTGCCA
 cDNA_rat 6701 GAGGTATCCTGGAGTTTGCCTGATGggacagtgcTCAACATGTAGCCCA
 genomic_hu 240 GAGATATCTTGGAGTTTGCCTGATGgaacoatgaTCAACATGCAATGCA
 cDNA_rat 6751 AGCTGATGACAGTGGCTATAGGACcaagaggtacACCCTTTTCACAATG
 genomic_hu 290 AGCCGATGACAGTGGCCACAGGACTaggagatatACCCTTTTCAACAATG
 cDNA_rat 6801 GAACCTTGTATTTCAACAACGTTGggatggcaGAGGAAGGAGATTATATC
 genomic_hu 340 GAACCTTTATACTTCAACAAGTTGgggtagcgGAGGAAGGAGATTATACT
 cDNA_rat 6851 TGCTCTGCCAGAACACCTTAGGGAAAGATGAGATGAAAGTCCACCTAAC
 genomic_hu 390 TGCTATGCCAGAACACCCTAGGGAAAGATGAAATGAAGGTCCACTTAAC
 cDNA_rat 6901 AGTTCTAACAGCcatcCCACGGATAAGGCAAAGCTACAAGACCACCATGA
 genomic_hu 440 AGTTATAACAGCtgotCCCCGATAAGGCAGAGTAACAAAACCAACAAGA
 cDNA_rat 6951 GGCTCaggGCTGGAGAAACAGCTGTCTTGAAGTGCAGAGTCACTGGGGaa
 genomic_hu 490 GAATCAaaGCTGGAGACACAGCTGTCTTGAAGTGTGAGGTCACTGGGGat
 cDNA_rat 7001 ccgaagoccaatgtATTTTGGTTGCTGCCTTCCAAcaatgtcatTTcATT
 genomic_hu 540 cccaaacccaaaaatATTTTGGTTGCTGCCTTCCAAatgaatgATTTCCTT
 cDNA_rat 7051 CTCCAATGACAGGTTTCAATTTTCATGCCAATagaaCTTTGTCCATCCATA
 genomic_hu 590 CTCCATTGATAGGTACACATTTTCATGCCAATgggtCTTTGACCATCAACA
 cDNA_rat 7101 AAGTGAAACCACTTGACTCTGGGGactatgtgtgcgtagctcagAATCCT
 genomic_hu 640 AAGTGAAACTGCTCGATTCTGGAGagtagtatgtgtagcccgAATCCC
 cDNA_rat 7151 AGTGGGGATGACACTAAGACATACAAACTGGAcattGTCTCTAAACCTCC
 genomic_hu 690 AGTGGGGATGACACCAAAATGTACAAACTGGatgtGTCTCTAAACCTCC
 cDNA_rat 7201 ATTAATCAATGGCCTGTATGCAACAaagACTGTTATTAAAGCCACAGCca
 genomic_hu 740 ATTAATCAATGGTCTGTATACAAACagaACTGTTATTAAAGCCACAGCtg
 cDNA_rat 7251 ttccggcacTCCAAAAAATACTTTGACTGCAGAGCAGATGGGATCCCATct
 genomic_hu 790 tgagacatTCCAAAAACACTTTGACTGCAGAGCTGAAGGGACACCATct
 cDNA_rat 7301 tcccaggtcacGTGGATTATGCCAGGCAATATTTTCCTCCAGCTCCATA
 genomic_hu 840 cctgaagtcacGTGGATCATGCCAGACAATATTTTCCTCACAGCCCCATA

00005120:042202

cDNA_rat	7351	CttTGAAGCAGAGTCACGGTCCATCCAAATGGAACCTTGGAgatgagga
genomic_hu	890	CtaTGAAGCAGAATCACAGTCCATAAAAATGGAACCTTGGAAattagga
cDNA_rat	7401	acatccGGCTTTCTGACTCTGCGGACTTCACCTGTGTGGttcggagcgag
genomic_hu	940	atgtgaGGCTTTTCAGATTACGCCGACTTTATCTGTGTGGcccgaaatgaa
cDNA_rat	7451	ggaGGAGAGAGTGTGTGGTAGTGACGTTAGAAGTCTTAGAAATGCTGAG
genomic_hu	990	ggtGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAARTGCTGAG
cDNA_rat	7501	AAGACCAACATTAGAAACCCATTCAACGAAAaagtcacgcgccaagctg
genomic_hu	1040	AAGACCGACATTTAGAAATCCATTTAATGAAAaagtagttgccagctgg
cDNA_rat	7551	gcaagcccgtAGCACTGAACTGCTCTGTGGATGGGAACCCCCACCTGAA
genomic_hu	1090	gaaagtccacAGCATTGAATTGCTCTGTGTGGTAACCCACCACTGAA
cDNA_rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTTGCTAACAGACCacacaa
genomic_hu	1140	ataatCTGGATTTTACCAAATGGCACAGATTTTCCAATGGACCacaaag
cDNA_rat	7651	ttccccGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTTACAAAgcaa
genomic_hu	1190	ttatcagTATCTGATAGCAAGCAATGGTTCTTTTATCATTTCTAAaocaa
cDNA_rat	7701	ctcggacaagtcAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGC
genomic_hu	1240	ctcgggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGC
cDNA_rat	7751	TAcacgagaaactcatcctgttagagATTGGGCAGAAGCCAGTCATTCT
genomic_hu	1290	TatattgagaaattagtcattattagaaATTGGCCAGAAGCCAGTTATTCT
cDNA_rat	7801	GACATACGAACCCAGGGatggtgaagagcgTCAGTGGGGAACCGTTATCAC
genomic_hu	1340	TACCTATGCACCCAGGGAcagtaaaaggoaTCAGTGGAGAATCTCTATCAC
cDNA_rat	7851	TGCATTGTGTCTGATGGgATCCCCAAGCCAAATGTCAAGTGGACTACA
genomic_hu	1390	TGCATTGTGTCTGATGGaATCCCTAAGCCAAATATCAATGGACTATG
cDNA_rat	7901	CCGGGTGGccATGTAATCGACAGGCCTCAAGTGGATGGAAAATACATAcT
genomic_hu	1440	CCAAGTGGtAtGTAGTAGACAGGCCTCAAATTAATGGGAAATACATAtT
cDNA_rat	7951	GCATGAAATGGCACGCTGGTCATCAAGCAACAACAGCtcacgaccaAG
genomic_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCttatgacagAG
cDNA_rat	8001	GAAATTATATCTGTAGGGCTCAAAACAGTGTGGCCAggaggttattagc
genomic_hu	1540	GAAACTATATCTGTAAGGCTCAAAATAGTGTGGTCatacactgattact
cDNA_rat	8051	gtgtCAGTGATGGTTGTGGCCTACCTCCCCGAATCATAAactacctACC
genomic_hu	1590	gttcCAGTAATGATTGTAGCCTACCTCCCCGAATTACAAatogtccACC
cDNA_rat	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCAetGTGTGG
genomic_hu	1640	CAGGAGTATTGTCAACAGGACAGGGGCAGCctttCAGCTCCACTGTGTGG
cDNA_rat	8151	CCTTGGGAATCCCCAAGCCaaAAGTCACCTGGGAGACGCCAAGACACTCC
genomic_hu	1690	CCTTGGGAGTTCCCAAGCCagAAATCACATGGGAGATGCCTGACCACTCC
cDNA_rat	8201	CTGCTCTCAaagcaacagcaagaaaaaccCATAGAAGTGAGATGCTTCA
genomic_hu	1740	CTTCTCTCAAcggcaagtaagagaggacacATGGAAGTGAGCAGCTTCA
cDNA_rat	8251	CCCACAAGGTACGCTgCTCATTGAGAATCTCCAAACCTCGGATTCCGGag
genomic_hu	1790	CTTACAAGGTACCTaGTCATTGAGAATCCCCAAACCTCCGATTCTGGga
cDNA_rat	8301	tcTATAAGTGCAGAGCTCAGAACCTACTTGGgacTGATTACGCAACAACT
genomic_hu	1840	taTACAAATGCACAGCAAGAACCCTTGGtagTGATTATGCAGCAACG
cDNA_rat	8351	TACATCCAGGTACTCTGACAGGAAGggggagactaaaattcaacagaagt
genomic_hu	1890	TATATTCAAGTAATCTGACATGAAataataaagtcacacaacatctgggca

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cDNA_rat 8401 ccacatocacagggTTTATTTTGGGAAGAAGTTAATCAAAGGCAGCCA
 genomic_hu 1940 gaa-----TTTATTTTGGGAAGAAGTTAATCAAAGGCAGCCA

 cDNA_rat 8451 TAGGCATGTAAATGAgtcTGAATACATTACAGTATTAAATTTACAATGG
 genomic_hu 1979 TAGGCATGTAAATGAatttGAATACATTACAGTATTAAATTTACAATGA

 cDNA_rat 8501 ACATGCgatga-----GACTTGTAATGAAAGCATTGTGAAGTGAaaccg
 genomic_hu 2029 ACATGCaaaataaaaagGACTTGTAATGAAAGCATTGTGAAGTGAatgata

 cDNA_rat 8546 agtctctg-----TGGATCTCAAAGCAAACCTTAACTTAAGGCACCTTTg
 genomic_hu 2079 ctgattttatttaaTGGATCTCAAACCAAACCTTAACTTAAGGCACCTTTt

 cDNA_rat 8591 ATTTTGGCCAACAAATAATAACAAACattaagagaaaaaatgattCACTA
 genomic_hu 2129 ATTTTGGCCAACAAATAACAATAAACaaacattgaaacgggtt----CACTA

 cDNA_rat 8641 CGAAATAACAAACGGCTAATGCACCTGAATTtctcagtaaaaagacotttc
 genomic_hu 2175 TAAATAACAAATGGCTAATGTACCTGAATTtttcagtaaaaaaatgaac

 cDNA_rat 8691 tctcgctaacagttgCCAGCTGCCTCGTGTCTGTTTCTACCAATGTGAC
 genomic_hu 2225 ttctaata-----CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTAC

 cDNA_rat 8741 AAACatogcacacagggTGAATGGAGTCAACGGGAAAGATTAAGTTTGCG
 genomic_hu 2268 AAGCATggcactca----GAACAGAGACAATGGAAATATTAATCTGCA

 cDNA_rat 8791 GTCTgtgtaaattctca-----ATGTACAAATATTCTGtcncTG
 genomic_hu 2314 ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG

 exon1 (2342-2397)
 cDNA_rat 8791 GTCTgtgtaaattctca-----ATGTACAAATATTCTGtcncTG
 genomic_hu 2314 ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG

 cDNA_rat 8829 GTTTATAAACATTTTGTATAAAACCGAAAAAAAAAAAAAAAAAAAAA
 genomic_hu 2360 GTTTATAAATTTTTTGTATAAACCTACAGAAATAAGcactgaactgtc

(Genomic human OCP: SEQ ID NO:4)
 (cDNA rat: SEQ ID NO:5)

24/90

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~231 7	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

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FIGURE 12

608 Human translated nucleotide sequence (ORF)

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGGTCTCCTTTGCTGT
GATCTGCCCTGGTCGCCACCCCTGGGGCAAGGCCTGCTCGCCGCTGTG
CCTGTTATATGCCTACGGAGGTACACTGCACATTTCCGGTACCTGACTTCCA
TCCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAAC
AGCTTGGTTAGATTGATGGAACAGATTTTCTGGCCTGACCAAACTGGA
GTTACTCATGCTTCACAGCAATGGCATTACACAATCCCTGACAAGACCTT
CTCAGATTTGCAAGCCTTGACAGGTCTTAAAAATGAGCTATAATAAAGTCC
GAAAACTTCAGAAAGATACTTTTTATGGCCTCAGGAGCTTGACACGATTG
CACATGGACCACAACAATATTGAGTTTATAAACCCAGAGGTTTTTATGG
GCTCAACTTTCTCCGCTGGTGCATTGGAAGGAAATCAGCTCACTAAGCT
CCACCCAGATACATTTGTCTCTTGGAGCTACCTCCAGATATTTAAAAATCTC
TTTCATTAAAGTTCCTATACTTGTCTGATAACTTCTGACCTCCCTCCCTCAA
GAGATGGTCTCCTATATGCCTGACCTAGACAGCCTTTACCTGCATGGA
CCCATGGACCTGTGATTGCCATTAAAGTGTTGTCTGACTGGATACAGCC
AGATGTAATAAAATGCAAAAAAGATAGAAGTCCCTCTAGTGCTCAGCAGT
GTCCACTTTGCATGAACCCCTAGGACTTCTAAAGGCAAGCCGTTAGCTATG
GTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCAACCATGACTCATCCCTG
AAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCT
CCCCAAGGTTTCATGGCACCCCTTTGGCTCCCTCACTTTGAATATGACAGAT
CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAGGCCCTCAAG
GACATCACCCATTGCATTCACTGAAGAAAATGACTACATCGTGCTAAATA
CTTCATTTTCAACATTTTGGTGTGCAACATAGATTACGGTCACATTACAGC
CAGTGTGGCAAAATTTGGCTTTGTACAGTGATTCTCCTCTGATACTAGAAA
GGAGCCACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAG
GTGGCTCCTAAGCCTGAAGACATTTTACCAACATAGAGGCAGATCTCAG
AGCAGATCCCTCTTGGTTAATGCAAGACCAAAATTTCTTGCAGCTGAACA
GAAGTGGCCACACATTCACTACATTACAGATCCAGTACTCCAGTGATGCT
CAAATCACTTTACCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGA
CTATGATTTCAAGGGATAACAATACTAAGCTGGAACATACTGTCTTGGTA
GGTGAACCGTTGGCCTGAACTGCCAGGCCAAGGAGACCCACCCACACA
CGTGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCTTATGTCA
GTGAGGATGGACGATCCTAATAGACAAAAGTGGAATTTGGAATCCA
GATGGCTGATAGTTTGACACAGGCGTATATCACTGTATAAGCAGCAATT
ATGATGATGCAGATACTCTACCTATAGGATAACTGTGGTAGAACCTTTGG
TCGAAGCCTATCAGGAAAATGGGATTCATCACACAGTTTTCATTGGTGAA
ACACTTGATCTTCCATGCCATTCTACTGGTATCCAGATGCCTCTATTAGC
TGGGTTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAA
AGTTCTAAACAATGGCACATTAAGAATATTACAGGTACCCCCGAAAGACC
AAGGTTATTATCGCTGTGTGGCAGCCAACCCATCAGGGGTTGATTTTTGA
TTTTCCAAGTTTCAGTCAAGATGAAAGGACAAAGGCCCTTGGAGCATGAT
GGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTATTGCTCATCT
TAAGGAGCCACCAAGGTGCACAACCTCCGTACATCTGCTCTGATGGAGGCTG
AGGTTGGAAAAACACACCTCAAGCACAAAGTAAGAGGCACAACATCGGGA
ATTAACTCCACGCGACGTGGAGATTCAACACATCGACGTTTATGGGAGA
ATAGGAGGCATTTCCTCCCTCTGCTAGGAGAATTGACCCACAACATTGG
GCGGCACTGTTGGAGAAAGCTAAAAAGAATGCTATGCCAGACAAGCGAG
AAAATACCACAGTGAGCCACCCCAAGTGGTCAACCAACTCCCAACATA
CCTGGTGAAGAAGACGATTCCCTCAGGCATGCTCGCTCTACATGAGGAATT

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TATGGTCCCGGCCACTAAAGCTTTGAACCTTCCAGCAAGGACAGTGACTG
CTGACTCCAGAACAATATCTGATAGTCCTATGACAAACATAAATTATGGC
ACAGAAATTCCTCCTGTTGTGAATTCACAAATACTACCACCTGAAGAACC
ACAGATTTCAAACGTGTCTACTGCTATTAATACTACAGCCATGTCAAAGAA
TATAAACCCAAACCATGTCAAGCCAAATACAAGGCACAACCAATCAACATT
CATCCACTGTCTTTCCACTGCTACTTGGAGCAACTGAATTTCAAGACTCTG
ACCAGATGGGAAGAGGAAGAGAGCATTTCCAAAGTAGACCCCCAATAAC
AGTAAGGACTATGATCAAAGATGTCAATGTCAAAATGCTTAGTAGCACCA
CCAACAACTATTATTAGAGTCAGTAAATACCACAAATAGTCATCAGACA
TCTGTAAGAGAAGTGAGTGAACCCAGGCACAATCACTTCTATTCTCACAC
TACTCAAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACACAGCTGC
TCATTCTCAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTT
CAGACGCTTTGGGAGGCAGAGGAAAATTGGCGGAAGGGGGCGGATTATC
AGCCCATATAGAACTCCAGTTCTGCGACGGCATAGATACAGCATTTTTCAG
GTCAACAACCAGAGGTTCTTCTGAAAAAAGCACTACTGCATTCTCAGCCA
CAGTGCTCAATGTGACATGTCTGTCTCTTCCCAGGGAGAGGCTCACCA
CTGCCACAGCAGCATTGTCTTTTCCAAGTGCTGCTCCCATCACCTTCCCCA
AAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCTACAACCTTAGTCCAG
AATCCACTATTACTACTTGAGAACAACCCAGTGTAGAGAAAAACAACACC
CACAATAAAATATTTCAAGGACTGAAATTTCCCAAGTGACTCCAACCTGGTG
CAGTCATGACATATGCTCCAACATCCATACCCATGGAAAAAACTCACAAA
GTAAACGCCAGTTACCCACGTGTGTCTAGCACCAATGAAGCTAAAAGAGA
TTCAGTGATTACATCGTCACTTTCAAGGTGCTATCACCAAGCCACCAATGAC
TATTATAGCCATTACAAGGTTTTCAAGAAGGAAAAATCCCTGGCAACAGA
ACTTTGTAAATAACCAATAACCCAAAAGGCAGATTAAAGGAATCAACATAAA
GTTAGTTTACAAAAAAGCACAGCTGTGATGCTTCTAAAACATCTCCTGCT
TTACCACAGAGACAAAGTTCCCTTTTCCATTTACCACACTTTCAACAAGT
GTGATGCAAATTCATCTAATACCTTGACTACCGCTCACCACTACGACC
AAAAACACAATCCTGGAAGTCTTCCAACAAGAAGGAGCTTCCCTTCCC
ACCCCTTAACCCCTATGCTTCCCTAGTATTATAAGCAAAGACTCAAGTACAA
AAAGCATCATATCAACGCAACAGCAATACCAGCAACAACCTCTACCTTC
CCTGCATCTGTCTCACTTATGAAACCCAAACAGAGAGATCTAGAGCACA
AACAAATACAAAAGAGAACAGGAGCCTCAAAAAGAAACAGGACTGACCCA
AACATCTCTCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACA
CCTCCTGCTCTGGCATTCACTCATTTCCCAACAGAAAAACAACCTGGGATT
TCAAGCACAATCAGTTTTTCAATCAAGAACTCTTAATCTGACAGATGTGATT
GAAGAACTAGCCCAAGCAAGTACTCAGACTTTGAAGAGCACAATTGCTTC
TGAAACAACCTTTGTCCAGCAAAATCACACCAGAGTACCACAACCTAGGAAAG
CATCATTAGACACTCCCATACCACCTTCTTGAGCAGCAGTGCTACTCTAA
TGCCAGTTCCCATCTCCCTCCCTTTACTCAGAGAGCAGTTACTGACACAC
GTGGCGACTCCCATTTCCGGCTTATGACAAATACAGTGGTCAAGCTGCAC
GAATCCTCAAGGCACAATCTCCAAATGCCAAGTTCACAATTGGAACCACT
CACTTCATCTACCTCTAATCTGTTACATTCTACTCCCATGCCAGCACTAAC
AACAGTTAAATCACAGAATTCCAAATTAACCTCATCTCCCTGGGCAGAAT
ACCAATTTTGGCACAAACCACTACTCAGACATTGCTGAAAAAGGCAAAAAG
CCAGAAGTAAGCATGTTGGCTACTACAGGCCTGTCCGAGGCCACCACTCT
TGTTTCAGATTGGGATGGACAGAAGAACACAAAGAAGAGTGACTTTGATA
AGAAACCAGTTCAAGAAGCAACAACCTCCAAACTCCTTCCCTTTGACTCTT
TGTCTAGGTATATATTTGAAAAGGCCAGGATAGTTGGAGGAAAAAGCTGCA
AGTTTTACTATTCCAGCTAACTCAGATGCCTTTCTTCCCTGTGAAGCTGTT

00005429 : 012200

GGAAATCCCCTGCCACCATTTCATTGGACCAGAGTTTCAGGACTTGATTTA
TCTAGAGGAAAACCAGAATAGCAGGGTCCAGGTTCTCCCAATGGTACCCT
GTCCATCCAGAGGGTGGAAATTCAGGACCGCGACAGTACTTGTGTCCG
CATCCAATCTGTTTGGCACAGACCACCTTCATGTCACCTTGTCTGTGGTTT
CCTATCCTCCCAGGATCCTGGAGAGACGTACCAAAGAGATCACAGTTCAT
TCCGGAAGCACTGTGGAAGTGAAGTGCAGAGCAGAAGGTAGGCCAAGCC
CTACAGTTACCTGGATTCTTGCAAACCAAACAGTTGTCTCAGAATCATCCC
AGGGAAGTAGGCAGGCTGTGGTGACGGTTGACGGAACATTGGTCCTCCAC
AATCTCAGTATTTATGACCGTGGCTTTTACAAATGTGTGGCCAGCAACCA
GGTGGCCAGGATTCAGTGTGGTTAAAAATACAAGTCATTGCAGCACCACC
TGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGCACTTGGGGTGAAA
GTTTAAACTGCCCTGTACTGCAAAGGAACTCCTCAGCCCAGCGTTTACT
GGGTCCTCTCTGATGGCACTGAAAGTGAACCAATTACAGTTTACCAATTCCA
AGTTGTTCTTATTTCAAATGGGACTTTGTATATAAGAAACCTAGCCTCTT
CAGACAGGGGCATTATGAATGCATTGCTACCAGTTCCACTGGTTCGGAG
CGAAGAGTAGTAATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGA
TAGAAGCTGCATCCCAGAAAAGGACTGAAGTGAATTTTGGGGACAAATTA
CTACTGAACTGCTCAGCCACTGGGGAGCCCCAAACCCCAAATAATGTGGAG
GTTACCATCCAAGGCTGTGGTCGACCAGTGGAGCTGGATCCACGTCTACC
CTAATGGATCCCCTGTTTATTGGATCAGTAACAGAAAAGACAGTGGTGTC
TACTTGTGTGTGGCAAGAAACAAAATGGGGGATGATCTGATACTGATGCA
TGTTAGCCTAAGACTGAAACCTGCCAAAATTGACCACAAGCAGTATTTTA
GAAAGCAAGTGCTCCATGGGAAAGATTTCCAAGTAGATTGCAAAGCTTCC
GGCTCCCCAGTGCCAGAGATATCTTGGAGTTTGCTGATGGAACCATGAT
CAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATAT
ACCCTTTTCAACAATGGAACTTTATACTTCAACAAAGTTGGGGTAGCGGA
GGAAGGAGATTATACTTGTATGCCCAGAACACCCTAGGGAAAGATGAA
ATGAAGGTCCACTTAACAGTTATAACAGCTGCTCCCGGATAAGGCAGAG
TAACAAAACCAACAAGAGAATCAAAGCTGGAGACACAGCTGTCCTTGACT
GTGAGGTCACTGGGGATCCCAAACCAAAAATATTTTGGTTGCTGCCTTCC
AATGACATGATTTCTTCTCCATTGATAGGTACACATTTTCATGCCAATGGG
TCTTTGACCATCAACAAAGTGAAGTGTCTGATTCTGGAGAGTACGTATG
TGTAGCCCGAAATCCCAGTGGGGATGACACCAAAATGTACAAACTGGATG
TGGTCTCTAAACCTCCATTAATCAATGGTCTGTATACAAACAGAAGCTGTA
TTAAAGCCACAGCTGTGAGACATTCCAAAAACACTTTGACTGCAGAGCT
GAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGACAATATTTT
CCTCACAGCCCCATACTATGGAAGCAGAATCACAGTCCATAAAAAATGGAA
CCTTGAAAATTAGGAATGTGAGGCTTTCAGATTACAGCCGACTTTATCTGTG
TGGCCCGAAATGAAGGTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTA
CTGGAATGCTGAGAAGACCGACATTTAGAAAATCCATTTAATGAAAAAT
AGTTGCCAGCTGGGAAAGTCCACAGCATTGAATTGCTCTGTTGATGGTA
ACCCACCACCTGAAATAATCTGGATTTTACCAAATGGCACACGATTTTCCA
ATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCA
TTTCTAAAACAACCTCGGGAGGATGCAGGAAAATATCGCTGTGCAGCTAGG
AATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAAATTGGCCAGAA
GCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAAGGCATCAGTGGAG
AATCTCTATCACTGCAATTGTGTGTCTGATGGAATCCCTAAGCCAAATATCA
AATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAATGGG
AAATACATATTGCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGC
TTATGACAGAGGAAACTATATCTGTAAGGCTCAAAATAGTGTGGTCATA

[illegible]

29/90
Figure 13

A

Region			Region Length	% identity	% positives	% gaps
General	Rat	Human				
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region			% identity	% positives	% gaps
Rat	Mouse	Length			
1-238	1-238	238	91	92	1

C

Region			Region Length	% identity
General	Rat	Human		
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region			Region Length	% identity
General	Rat	Mouse		
1-720	1-718	1-720	720	93

2025-04-06 15:06:00

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rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
CGAGAGACGACAGAGAGTTACCGCTCGCAGAGACGACAGAGGGTCCAGAAAAAGGAAA
-----
CAGAGGGTCCAGGAAA-GGAAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
GTGCTGGAGGGGAGTGGGGACAAAAGCAGCGAOCAGTGAATGTCACTTCAGTGACTGAG
-----
GTACTGGAGGGGAGTGGGGACAAAAGCAGCGAOCAGGGAACATCGCTTCAGTGACTGAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
GCCAGGCAAAAACGCGCGGGAAGGATTTTGTGTAGCTTGGGACCCCTTCATAGACACTGAT
-----
GCCAGGCAAAAAGGAGCGGGGAAGGATTATATGTAGCTGGGAGCGCTTCATAAACACTGAT

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
GACACGTTTACGCAAAATA-GAAATTTGAGGAGAAAACGCTGGGCCTTOGGAAAG---GA
-----
GACGTGTTTGTGCAAGCAGACGAAATTTGAGGAGAAAACGCTGGGAGCTCGGAAAGAAGGA

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
GTGATTGATTAGTACTTGCAGTTTAGGTGACTTTAAGGAGAACTAACTAATGTATACTA
-----
GTGATCGATTAGTACTTGTAGTTTAGGTGAGTTT---GAGRACTAACTAACTATACTA

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
TTGAGGGAGGAGGAAGAGCATTACAGAGTTTCCAGCAGCAGCGGAAAGCTTTGTTAAT
-----
TTGAGGGAGGAAGGAAGAGCATT-----CCAGCAGCAGCAGGAAAGCTTTGTTAGT

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
TTGGAAATGGATGATAGCATTAAATAACAGAAGCGCCTCCAGGTCTCTGAAGCTTCAGT
-----
TTGGAAATGTATGATACCATTAATAATAACAGAAGCGCCTCCAGTCTCTGAAGAGTCAGT

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
CCCCCAGCTGAAAGCCAGAAAAGACTAAGCCCTAAGCCCTTTTGATCCCTTTGGAAGCA
-----
CCCCCAGCT-----A-GTGTAGCCTACTAAGCCTTTTGCTCCCGTTGGAAGCA

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
AAGAACTTTCCTTCCCTGGGGTGAAGACTCTCTCAGAAAGATTCTCTCTGCTATG
-----
AAGAACTTTCCTTCAATCAGGTGAAGGCTCTCTCAGAAAGATTCTCTCTGCTATG

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
TTACAGAGGAATCAAACCAAGACAGAAGAGCTCAGGATGCAAGGTGAGAGGCAGGGAAG
-----
ATGAAGGTAAAAGGCAGAGGAA
TTACAGAGGATTCAAAGCAAGACAGAAGAGCTCAGGATGCAGAGAGAGGCAGGGAAG
*** ** * ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
TCAGCGGCTTGTGATCTCCCTCACTGCTGTCTGCTGGTGGTCAACCCCTGGGAGCAGGG
-----
TCACTGCTGTGCTGGTCTCCCTTGTCTGTGATCTGCTGGTGGTCAACCCCTGGGAGCAGG
TCAGCTGCTGTGCTGATCTCCCTCACTGCCATCTGCTGGTGGTCAACCCCTGGGAGCAGGG
*** * ***** ** ***** ** ***** ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
CCTGTCTCTCGCGGCTGTGCTGTCTATGTGCCCACAGAGGTGCACTGTACATTTGGGTACC
-----
CCTGTCTCTCGCGGCTGTGCTGTCTATGTGCCCACAGAGGTGCACTGTACATTTGGGTACC
TCTGTCTCTCGCGGATGTGCTGTCTATGTGCCCACAGAGGTGCACTGTACATTTGGGTACC
***** ***** ** ***** ** ***** ***** *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5
-----
TGACCTCCATCCAGATGG-CATCCCGGCCAATGTGGAACGAATAAATTTAGGATATAAC
-----
TGACCTCCATCCAGACAG-CATCCCGGCCAATGTGGAACGCATCAATTTAGGATATAAC
TGACCTCCATCCAGAGCGGGCATCCAGGCCAATGTGGAACGAGTCAATTTAGGATATAAC
*** ***** * ***** ***** ***** ***** *****

```

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AGCCTTACTAGATTGACAGAAAAAGACTTTGATGGCCTGAGCAAACTGGAGTTACTCATG
AGCTTGGTTAGATTGATGGAAACAGATTTTCTGGCCTGACCAAACTGGAGTTACTCATG
AGCCTCACTAGATTGACAGAAAAAGACTTTTCTGGCCTGAGCAGACTGGAGTTACTCATG
*** * ***** ** * ***** ** *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTGCACAGTAATGGCATTACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTGCTTG
CTTCACAGCAATGGCATTACACCAATCCTGACAGACCTTCTCAGATTGTCAGGCGTTG
CTGCACAGCAATGGCATTACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTGCTTG
** ***** ** *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CAGGTCTTAAAAATGAGCTATAACCAAGTCCAAATCATTGGGAGGATACTTTCTACGGA
CAGGTCTTAAAAATGAGCTATAATAAAGTCCGAAACCTTCAGAAAGATCTTTTATGGC
CAGGTCTTAAAAATGAGCTATAACCAAGTCCAAATCATTGAGAGGATACTTTGATGGA
***** ** * *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTCGGAGCTTGGTCCGGTTGCACTGCAATCAACAACATTGAATTCATCAACCTGAG
CTCAGGAGCTTGACAGATTGCACTGCAATCAACAACATTGAATTCATCAACCTGAG
CTCAGGAGCTTGACAGATTGCACTGCAATCAACAACATTGAATTCATCAACCTGAG
*** ***** ** *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GCTTTTATGGACTTACCTCGCTCCGCTTGGTACATTAGAAGGAAACCGGCTCACAAG
GTTTTTATGGGCTCACTTTCTCCGCTTGGTACATTAGAAGGAAACCGGCTCACAAG
GCGTTTTACGGACTCACCTTGGCTCCGCTTGGTACATTAGAAGGAAACCGGCTCACAAG
* ***** ** * *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTCCATCCAGACACATTGTCTCTTAAGCTATCTCCAGATATTTAAACCTCTTTTCATT
CTCCATCCAGATACATTGTCTCTTTGAGCTACCTCCAGATATTTAAACCTCTTTTCATT
CTCCATCCAGACACATTGTCTCTTTGAGCTATCTCCAGATATTTAAACCTCTTTTCATT
***** ** * *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGTACCTGTCTGTCTGATAACTTCTT-GACCTCCCTCCCAAAGAAATGGTCTCCTA
AAGTCTCTATCTGTCTGATAACTTCTT-GACCTCCCTCCCTCAAGAGATGGTCTCCTA
AAGNACCTGTCTGTCTGATAACTTCTT-GACCTCCCTCCCAAAGAAATGGTCTCCTC
*** * *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CATGOCAAACCTAGAAAGCCTGTATTGTCATGGAAACCATGGACCTGTGACTGCCATT
TATGCTGACCTAGACAGCCTTTACCTGTCATGGAAACCATGGACCTGTGACTGCCATT
TATGOCAAACCTAGAAAGCCTTTACTTGTATGGAAACCATGGACCTGTGACTGCCATT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAAGTGGTTGTCTGAGTGGATGCAGGGAACCCAGATATAATAAAATGCAAGAAAGACAG
AAAGTGGTTGTCTGACTGGATACAGGNNNNOCAGATGTAATAAAATGCAAAAGATAG
AAAGTGGTTGTCCGAGTGGATGCAGGGAACCCAGGTA-ACTATCTTGT-TTGTGTTG
***** ** *****

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGCTCTTCCAGTCTCAGCAATGTCCCT-TTGATGAACCCAGGATCTCTAAAGGCA
AAGTCCCTCTAGTCTCAGCAGTGTCCCT-TTGATGAACCCAGGATCTCTAAAGGCA
TTTCTTTTTTATARKAGTATTTCTCAATTTCAATTTAGAAATGATATCCAAAGTCT-
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GACCTTTGCTATGGTACCATCTGGAGCTTTCTATGTACAAAGCCACCATTTGATCCAT
AGCCGTTAGCTATGGTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCACCATTTGACTCAT
-CCCATAACTCCCTCCCA-CTTCCCTACCTACCATTC-CCATTTTGTGGC
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CAGTGAAGTCAAAGAGCCTGGTTACTCAGGAGGACATGGATCTGCTCCACTCACTC
CCTGAAATCAAAGAGCCTGACTATTCTGGAGACAGTAGTTCTGCTTTCTCTCTCCCC
CCTGGCATTCCTC-----
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGATTTATAGAACCTTTGGCTCCTGTCTTTGAACATGACANNTNTCTGGAATA
AAGTTTCAATGGCACCTTTGGCTCCTCATTGAAATATGACAGATCAGTCTGGAATG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AGGCGACATGGTCTGTAGTATCAAAAGCATCAAGGACATCAACCACTGCATTCACTG
AAGCTAATCATGGTCTGTAGTATCAAAAGCCTCAAGGACATCAACCACTGCATTCACTG

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rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGAAAAATGACTACATCATGCTAAATGGGTCAITTTCCACAAATCTTGTGTGCAGTGTAG
AAGAAAAATGACTACATCGTGTAAATACTTCATTTTCAACATTTTGGTGTGCACATAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ATTATAATCACATCCAGCCAGTGTGGCACTTCTGGCTTTATACAGTGACTCTOCTCTGA
ATTACGGTCACATTCAGCCAGTGTGGCAAATTTTGGCTTTGTACAGTGATTCTOCTCTGA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TACTAGAAAGGAAGCCCCAGCTTAOCGAGACTCCTTCAGTGTCTTCTAGATATAAACAGG
TACTAGAAAGGAGCCACTTGCTTAGTGAACACCCGAGCTCTATTACAATATAAACAGG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGGCTCTTAGGCOCTGAAGACATTTTACCAGCATAGAGGCTGATGTGAGAGCAGACCOCTT
TGGCTOCTTAGGCOCTGAAGACATTTTACCAGCATAGAGGCTGATGTGAGAGCAGATCOCT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TTTGGTTCCACACAGAAAAATTTGTCTTG CAGCTGAACAGAACTGCCACCACTTAGCA
CTTGGTTAATGCAAGACCAAATTTCTTG CAGCTGAACAGAACTGCCACCACTTAGCA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CATTACAGATCCAGTTTTCCACTGATGCTCAAATCGCTTTACCAAGGGCGGAGATGAGAG
CATTACAGATCCAGTACTCCAGTGAATGCTCAAATCACTTTACCAAGAGCAGAGATGAGGC

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CGGAGAGACTCAAATGGACCATGATCTGATGATGAACAAATCCAAACTGGAAAGCACTG
CAGTGAACACAAATGGACTATGATTTCAGGGATAACATACTAAGCTGGAACTACTG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TCTTGGTTGGCGGCACTATTGCOCTGAGCTGTCCAGGCCAAAGGCGAOCCTTCAOCTCACT
TCTTGGTAGGTGGAAOCTTGGCTGAACTGCCAGGCCAAGGAGACCCACCCACAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCOCTTACGTTAGGAGGATGGGC
TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCOCTTATGTCACTGAGGATGGAC

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GAATCCTAATAGACAAAAATGGGAAGTTGGAAGTGCAGATGGCTGACAGCTTTGATGCAG
GGATCCTAATAGACAAAAATGGGAAGTTGGAAGTGCAGATGGCTGATAGTTTTCACACAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GTCITTACCACTGCATAAGCAOAAATGATGCAGATGGGATGTTCTCACATACAGGATTA
GCGTATATCACTGTATAAGCAGCAATTATGATGATGCAGATATTCTCACCTATAGGATAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTGTGGTAGAGCOCTATGGAGAAAGCACATGACAGTGGAGTCCAGCACAGTGGTTA
CTGTGGTAGAGCOCTTTGGTCCAGGCTATCAGGAAATGGGATTCATCACACAGTTCATCA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CGGGTGAGAGGCTGAGCCTTCATGCTTTCCAGGGTGTTCAGATGCTTCTATTAGCT
TTGGTGAAACACTTGATCTTCATGCTTTCTACTGGTATCCAGATGCTTCTATTAGCT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GGATTCTTCAGGGAACACTGTGTTCTCTCAGCCATCAAGAGACAGGCAATTCITAACA
GGGTTATTCCAGGAAACATGTGCTCTATCAGTCATCAAGAGACAGGCAATTCITAACA

0005120-012202

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATGGGACCTTAAGAATATTACAGGTTACGCCAAAGATCAAGGTCATTACCAATGTGTGG
ATGGCACATTAAGAATATTACAGGTCACCCCGAAAGACCAAGGTTATTATCGCTGTGTGG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGCCAACCCATCAGGGGCGGACTTTTCCAGTTTAAAGTTTCAGTTCAAAGAAAGGCC
CAGCCAACCCATCAGGGGTTGATTTTGTATTTCCAGTTTCAGTCAAGATGAAAGGAC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AAAGGATGGTTGAGCATGACAGGGAGGCGAGGTGGATCTGGACTTGGAGAACCCAACTCCA
AAAGGCCCTTGGAGCATGATGGAGAACAGAGGGATCTGGACTTGTATGATGATCAATCCTA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GTGTTTCCTTAAGCAGCCAGCATCTTTGAACTCTCTGCATCAGCTTTGACAGGGTCAG
TTGCTCATCTTAAGGAGCCACAGGTGCACAACTCCGTACATCTGCTGTATGGAGGCTG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AGGCTGGAAACAGTCTCCGGTGTACATAGGAAGAACAAACATAGAGACTTAATACATC
AGGTTGGAAACACACCTCAAGCACAAAGTAAGAGGCACAACTATCGGAATTAACACTCC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GGCGGCGTGGGGATCCACGCTCCGGGCAITCAGGAGCATAGGAGGCAGCTCCCTCTCT
AGCGAOGTGGAGATTCAACACATGACGTTTTAGGGAGAAATAGGAGGCATTTCCTCCCT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGCTCGGAGAATTGACCCGCAACGCTGGGCAGCACTTCTAGAAAAGCCAAAAGATT
CTGCTAGGAGAATTGACCCACAACTTGGGGGCACTGTTGGAGAAAGCTAAAAGAAATG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGTGCCAAAAGCAAGAAAATACCAAGTAAGCCAGTGCCACTGGCTGTTCCCTCG
CTATGCCAGACAGCGAGAAAATACCAAGTGAGCCCAACCCAGTGGTCAOCCAACTCC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TGGAACCTCACTGACGAGGAAAAGGATGCTCTGGCATGATTCCTCCAGATGAAGAATTCA
CAAACATACCTGGTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAATTAA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TGGTTCTGAAACTAAGGCTTCTGCTGTCCAGGAAGGTCAOCCACTGCTGACTCTGGAC
TGGTCCCGGCCACTAAGCTTTGAACCTTCCAGCAAGGACAGTGACTGCTGACTCCAGAA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CAGTAAATCATGGTTTTATGACGAGTAAGCTTCTGGCACAGAGTCTCAACTGTGAATC
CAATATCTGATGCTCTATGACAAACATAAATTATGGCACAGAACTCTCGTTGTGAATT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CACAAACACTACATCTGAGCACCTTCTGATTTCAAAATTATTAGTGTAAACAAAGGTA
CACAAATACCTACCACTGAGGAACCCACAGATTTCAAAGTGTCTACTGCTATTAACAACTA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CAGCTGTGACAAAGAGTATGAACCATCCATAGCAAGCAAAATAGAAGATACAAACCAAC
CAGCCATGTCAAAGATATAAACCCCAACCATGTCAAGCCAAATACAAGGCACAAACCAATC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AAAACCCAAATCATTATCTTTCATC-----AGTAGCTGAATTCGAGATTCTG-CT
AATATTATCCACTGTCTTTCCTACTGCTACTTGGAGCAACTGAATTCAGGACTCTGACA

00005139-0122002

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGCA---GGAAGAGCATCTTCCAAAGTGCACACCTGTAAAGGGGAAACATGGCT
GAGGGAAGAGGAAGAGAGCAITTC---AGTA-ACCCCCAATAACAGTAAGGACTATGATC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACCTATGGGCATACCAACACATA--TAGTAGCTTTACAGCAAAGCCAGTACAGTCTTGC
AAAGATGNTCAATGTCAAANATGCTTAGTAGCCACCAACAAA-CTATTA-----TTAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AGCCATAAATCCAACGAAAGTTATGGACCTCAGATACCTATTACAGGAGTCAGCAGAC
AGTCAGTAATAACCAAAATAGTCAT-----CAGACATCTGTAGAGAAGTGAAGTGAAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CTAGCAGTAGTGACATCTCTTCTCACACTACTGCAGACCTAGCTTCTCCAGTCAACCTT
CCAGGCACAAATCCTTCTATTCTCACACTACTCAAATACTTAGCACTCCAGTTCCCTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGTTCCACACCACTGCTCTTTATTTTACATTCCTAGAAACAACAATACAGGTA
CAGATCCACACACAGCTGCTCATTTCTAGTTTCOGATCCCTAGANNNAATAGTACAGTTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACTTCCCTTGTCCAGGCACTTGGGAAGAGAGAGACAATTTGGAGCAGAGGGAGAGTTA
ACATCCCGCTGTTCAGAGCTTTGGGAGGCAGAGGAAATTTGGCGGAGGGGGGAGTTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AAAACCCACATAGAACCCAGTTCTCCGACGGCATAGACACAGGACTGTGAGGCCAGCAA
TCAGCCCATATAGAACTCCAGTTCTCGGACGGCATAGATACAGCAITTTTCAAGTCAACAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGGGGACCTGCTAACAAAATGTGAGCCAGTTCCAGCCACAGAGTACCTGGGATGT
CCAGAGGTTCTTCTGAAAAAGCACTACTGCATTTCTCAGCCACAGTCTCAATGTGACAT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCCACACATGTCTTCCGAGAGGGGCTCAGTGGCTACTGCAGCACTGTCAGTTCCAA
GTCTGTCTGTCTTCCAGGGAGAGGCTCACCACTGCCACAGCAGCATTTGCTTTTCCAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GTTCAATCCACAGTGCCCTCCCAAACTAATAATGTTGGGGTCATAGCAGAAGAGTCTA
GTCTGTCTCCATCACTTCCCAAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCTA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CCACTGTGGTCAAGAAACCACTGTACTATTTAAGGACAAACAAATGTAGATATTGAGA
CAACTCTAGTCCAGATCCACTATTACTACTTGAGAACAAACCCAGTGTAGANNNGAAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TAATAACAACCACTACAAAATATTCGGAGGGGAAAGTAACCAAGTGATTCTACGGAA
NNACACACCCACAATAAATATTCAGGACTNGAAATTTCCCAAGTGACTCCAACCTGGT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAAGCATGACTTCTGCTCCACATCTGTATCCCTGGGGAAATCTCCTGTAGACAATAGTG
CAGTCATGACATATGCTCCACATCCATACCCATGGAAAAAATCCAAAGTAAGGCCA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GTACCTGAGCATGCTGGGAACATCCAACTGGGAAAGATTGAGTGAAACACACACCAC
GTTACCCAGCTGTCTAGCAACAAATGAAGCTAAAGAGATTGAGTGATTACATGCTCAC

00005430-012000

TTCCAGGCCCCCTCAGCACCCCTCAATACCAA-----CAAGCCAAAATTCTCAAGA
TTTCAGGTGCTATCACCAAGGCCCAATGACTATTATAGCCATTACAGGTTTTCAGAA

GGAAACTCCCTTGCACAGATCTTTGTAAATAACAGAGAAGGGGGGATGTTAAGA
GGAATAATCCCTGGCAACAGAACTTTGTAAATAACCAATAACCAAGGCAGATTAA

ATCCATATCAATTGGTTTACAAAAGAACCCAGCGCAAAGOTTCCCAAATAGCTCTC
ATCAACATAAGTTAGTTTACAAAAGACAGAGTGTGATGCTTCTTAAACATCTCTG

TTTACCCACAG-GTCAGAGTTCCCCCTCAGATTCTACAACTCTCTTGACAAGTCCGCA
CTTAC-ACAGAGACAAGTTCCCTTTCCATTTCACACACTTTCAACAAGTGTGATG

CCAGCTCTGTCTACAACAATGGCTGCCACTCAGAACAGGGGCACTGAAGTAGTATCAGGT
CAAATTCACCTAATACTTGTACTACGGCTCAACCACTACGACCAAA--ACACACA-T

GCCAGAAGTCTCTCAGCAGGGAAGAAGCAGCCTTCAOCAACTCTCTCAG-TGCTTC
CCTGGAGTCTTCAACAAAGAGGAGCTTCCTTC-CCACCCCTTACCCCTATGCTTC

TAGCACCATAGCAAGAGATCTAATACATTAACTTCTTGTCAACGGAAACCCOCACAGT
 TAGTATTATAAGCAAGACTCAGTACAAAAGCATCATATCAACGCAACAGCAACGCG

GACAAGTCCTACTGCTACTGCTATGTGTCATTATGTCTGAAACCAACGACAAAGATCCAA
AACAACCTCCTACCTTCCCTGCATCTGTGTCATCACTTATGAAACCAACACGAGAGATCTAG

AGAGCGAAAAGACCAATAAGGGGCGCTCG--GAAGACAGAAACACGCAACAACAC
AGCACAACACATACAAAGAGAGGAAGCTCAAAGAAGACAGGACTGACCCAAACATCTC

CCCCAGGCAGGTTTCTGGCTAAGTGCATACTCAGCTCTACACAGCTGATACCCCCCT
TCCAGACCCAGAGTTCTGGCTTCACTACACCCACTGCTATGACCACTCTCTNGCTCTNN

GGCTTCAGTCATTCCOCCACGACAGATGATGGTGGAAATGTAAGTGCAGTTGCTTTATCA
NGCATTCACTCATTCCOCCACGAGAAAACACAACACTGGGATTTCAGACACATCAGTTTTCA

CTCAACAACCTCTCTTCTGGCCA---TAACTGAAGTGTTTGAG-AGGTAC--AOCAGAC
TTCAAGAAGCTCTTAATCTGAACGATGTGATTGAAGAACTAGCCCAAGCAAGTACTCAGAC

TTTGGGAATACACACGCTTTGGAAACAACGTTGTTGAGCAAATCACAGGAGGTACCAC
TTTGAAGAGCACAAATGCTTCTGAACAACACTTTGTCCAGCAAATCACACCAGGTACCAC

AGTGAAGAGAGCTCA---GACAC---ACCAACCACTCTCTCAGCAGTGGGGGCGCCCG
AATAGGAAGAGCATCATTAGACACTCAACCAACCACTTCTTGAGCAGCAGTGTCTACTT

[illegible]

CTGTGGT TTTTACCGSCAAGGATTTTGGACAGACATGTCAAGGAGATCACAGTTTCACT
CTGTGGT TTTCTATCTCTCCAGGATCTGGAGAGAAGTACCAAGAGATCACAGTTTCACT

TTTGAAGTACTGTGGAACTAAGTGCAGAGTGGAGGGTATGCCGAGGCGCTACGGTTTCT
CCGGAAGCACTGTGGAACTGAAGTGCAGAGCAGAAGGTAGGCCAAGCGCTACAGTTA

GGATACCTTGCAAACCAAACGGTGGTCTCAGAAACGGCCAGGGAAGCAGAAAGGTCTGGG
GGATTCCTTGCAAACCAAACAGTTGTCTCAGAAATCATCCAGGGAAGTAGGCAGGCTGTGG

TAACAACCTGATGGAACATTGATCATCTATAATCTGAGTCTTATGATOGTGGTTTTTACA
TGAOGGTTGACGGAACATTGGTCTCCACATCTCAGTATTTATGACOGTGGCTTTTACA

AGTGTGTGGOCAGCAACCCATCTGGOCAGGATTCACCTGTTGGTTAAGATACAAGTCATCA
AATGTGTGGOCAGCAACCCAGGTGGOCAGGATTCACCTGCTGGTTAAATACAAGTCATTG

CAGCTOCCCCGTGTCATTATAGAGCAAAGAGGCAAGCCATCGTTGGGGTTTtaggtggaa
CAGCACACCTGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGCACTTGGGGTGAAA

GTTTGAAACTGCCCTGCACTGCAAAAGGAACTCCCGAGCTAGTGTTCACTGGGTCTTT
GTTTAAAACTGCCCTGTACTGCAAAAGGAACTCCTCAGCCGAGCGTTTACTGGGTCTCT

ATGATGGGACTGAACTAAAACATTGCAGTTGACTCAATOCAGATTTTTCTGTATOC
CTGATGGCACTGAAGTGAACATTACAGTTTACCAATTOCAAGTTGTTCTTATTTTCAA

ATGGAACCTCTGTATATAAGAAGCATCGCTCCTTCAGTGGGGGCACTTATGAGTGCATTG
ATGGGACTTTGTATATAAGAAACCTAGCCTCCTTCAGACAGGGGCACTTATGAATGCATTG

CCACAGCTCCTCAGGCTCAGAGAGAAGGGTAGTGATTCTTACTGTGGAAGAGGGAGAGA
CTACCACTTCCACTGGTTCCGAGOGAAGAGTAGTAATGCTTACAATGGAAGAGOGAGTGA

CAATCCCCAGGATAGAACTGCTCTCAGAAATGGACTGAGGTGAATTTGGGTGAGAAAT
CCAGCCCCAGGATAGAACTGCATCCAGAAAGGACTGAAGTGAATTTGGGGACAAAT

TACTACTGAACTGCTCAGCTACTGGGGATCCAAAGCCTAGATAATCTGGAGGCTGCCAT
TACTACTGAACTGCTCAGCCACTGGGGAGGCCAATCCCAATAATGTGGAGGTTAACCAT

CCAAGGCTGTCTATGACCAAGTGGCA CAGAATGGGCAGCCGATCCACGTCTACCCAAATG
CCAAGGCTGTGGTCGACCAAGTGG-----GCAGCTGGATCCACGTCTACCCCTAATG

GATCCTTGGTGGTGGGTCACTGACGGAARAAGACGCTGGTGACTACTTATGTGTGGCAA
GATCCCTGTTTATTGGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCAA

GAAACAAAATGGGAGATGACCTAGTCTGATGCATGTCCGCCTGAGATTGACACCTGCA
GAAACAAAATGGGGGATGATCTGATACTGATGCATGTTAGCCTAAGACTGAAACCTGCCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 AAATTGAACAGAAAGCAGTATTTTAAAGCAAGTGCTCCATGGGAAAGATTTCOAAGTGG
 AAATTGAACACAGCAGTATTTTAAAGCAAGTGCTCCATGGGAAAGATTTCOAAGTAG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 ACTGCAAGGCTCTGGCTCCCTGTGCTGAGGTATCTGGAGTTTGCTGATGGGACAG
 ATTGCAAAGCTTCCGGCTCCCACTGCCAGAGATATCTTGGAGTTTGCTGATGGAAOCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TGCTCAACAATGTAGCCCAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCCCTT
 TGATCAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATATACCCCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TCCACAATGGAACTTGTATTTCACAACGTTGGGATGGCAGAGGAGGAGATTATATCT
 TCAACAATGGAACTTTATACCTTCAACAAGTTGGGGTAGGGAGGAGGAGATTATACCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GCTCTGCCAGAACACCTTAGGGAAAGATGAGATGAAGTCCACCTAACAGTTCTAACAG
 GCTATGCCAGAACACCTTAGGGAAAGATGAATGAAGTCCACTTAACAGTTATAACAG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCATCCACGGATAAGGCAAAGCTACAGACCCATGAGGCTCAGGGCTGGAGAACAG
 CTGCTCCCGGATAAGGCAGAGTAACAAACCAACAGAGAAATCAAAGCTGGAGACACAG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CTGTCTTGACTGCGAGGTCACTGGGAAACGAAGCCCAATGTATTTTGGTTGCTGCCTT
 CTGTCTTGACTGTGAGGTCACTGGGATCCCAAACCAAAATATTTTGGTTGCTGCCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCAACAATGTCAATTCATTCCTCAATGACAGGTTCAATTTCTAGCCAATAGAACTTTGT
 CCAATGACATGATTTCTCTCCTATGATAGGTACACATTTCTAGCCAATGGGTCTTTGA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCATCCATAAAGTGAAACCACTTGACTCTGGGACTATGTGTGCGTAGCTCAGAACTCTA
 CCATCAACAAGTGAAACTGCTCGATTCTGGAGAGTAOGTATGTGTAGCCCGAAATCCCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GTGGGGATGACACTAAGACATACAACTGGACATTTCTCTAAACCTCCATTAAATCAATG
 GTGGGGATGACACCAAAATGTACAACTGGATGTGGTCTCTAAACCTCCATTAAATCAATG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GCCTGTATGCAACAAGACTGTTATTAAAGCCACAGCCATTGGGCACTCCAAAAAATACT
 GTCTGTATACAAACAGAACTGTTATTAAAGCCACAGCTGTGAGACATTCAAAAAATCACT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TTGACTGCAGAGCAGATGGGATCCCATCTTCCAGGTCAAGTGGATTATGCCAGGCAATA
 TTGACTGCAGAGCTGAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGACATA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TTTTCTCCAGCTCCATACTTTTGGAGCAGAGTCACGGTCCATCCAAATGGAACCTTGG
 TTTTCTCCAGCTCCATACTTTTGGAGCAGAGTCACGGTCCATCCAAATGGAACCTTGG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 AGATGAGGAACATCCGGCTTTCTGACTCTGCGGACTTCACTGTGTGGTTCCGAGCGAGG
 AAATTAGGAATGTGAGGCTTTCAAGATCAGCCGACTTTATCTGTGTGGCCCGAAATGAAG

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rat_cDNA
human_5+3_corrected
mus_cDNA_5

GAGGAGAGAGTGTGTTGGTAGTGCAGTTAGAAGTCTAGAAATGCTGAGAAGAACACAT
GTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGAAACCCATTCAACGAAAAAGTCATGCOCAAGCTGGCAAGCCCGTAGCACTGAACT
TTAGAAATCCATTTAATGAAAAATAGTTGCCAGCTGGGAAAGTCCACAGCATTGAATT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

GCTCTGTGGATGGGAACCCCACTGAAATTAOCTGGATCTTAOCTGAOGGCACACAGT
GCTCTGTGATGGTAACCAOCCOCTGAAATAATCTGGATTTTAOCAAATGGCACACAGT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TTGCTAACAGAACACACAATTCCOOGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTT
TTTCCAAATGGACACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCATT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACAAAGCAACTGGGAACAAGTCAGGGAGATATCGCTGTGCAGCCAGGAATAAGGTTGGCT
CTAAACAACACTGGGAGGATGCAGGAAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACATCGAGAAACTCATCTGTAGAGATTGGGCAGAGCCAGTCAATCTGACATAOGAAC
ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAGCCAGTTATTCTTACCTATGCAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

CAGGGATGGTGAAGAGCGTCAGTGGGGAACCGTTATCACTGCATTGTGTCTGATGGGA
CAGGGACAGTAAAGGCCATCAGTGGAGAATCTCTATCACTGCATTGTGTCTGATGGAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCCCCAAGCCAAATGTCTAGTGGACTACACCGGGTGGCCATGTAATGACAGGCTCAAG
TCCCTAAGCCAAATATCAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCTCAAA

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TGGATGGAAATACATCTGCATGAAATGGCAOCTGGTCATCAAAGCAACACAGCTC
TTAATGGGAATACATATTGCATGACATGGCACCCTTAGTCATTAAAGAGCAACAGCTT

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ACGAOCAGGAAATATATCTGTAGGGCTCAAAACAGTGTGGOCAGGCAATTATTAGCG
ATGACAGAGGAACTATATCTGTAAGGCTCAAAATAGTGTGGTCATACACTGATTACTG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TGTCAGTGATGGTTGTGGCTACCTCCCCGAATCATAAACTAOCCTAOCAGGAACATGC
TTCCAGTAATGATTGTAGCCTACCTCCCCGAATTACAAATGCTOCACCCAGGAGTATTG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

TCAGGAGGACAGGGGAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA
TCACCAGGACAGGGGACGCCCTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG

rat_cDNA
human_5+3_corrected
mus_cDNA_5

AAGTCACCTGGGAGACGCCAAGACACTCCCTGCTCTCAAAAGCAACAGCAAGAAAACCCC
AAATCACATGGGAGATGCTGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGACAC

rat_cDNA
human_5+3_corrected
mus_cDNA_5

ATAGAAGTGAGATGCTTCACCCACAAGGTACGCTGGTCATTGAGAAATCTCCAAACCTCGG
ATGGAAGTGAGCAGCTTCACTTACAAGGTACCTAGTCATTGAGAAATCCCCAACTCCG

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ATTCCGGAGTCTATAAGTGCAGAGCTCAGAACTACTTGGGACTGATTACGCAACAACCTT
ATTCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAAAGT

ACATCCAGGTA CTCTGACAGGAAGGGGAGACTAAAATTCAACAGAAGTCCACATOCACA
ATATTCAAGTAATCTGACATGAA-----ATAATAAAGT-CAACAA-----CATCTGGGCA

GGGTTTATTTTTGGAAGAAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAGTCTGA
GAAATTATTTTTGGAAGAAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAATTTGA

ATACATTACAGTATTAAATTACAAATGGACATGCGA--TGA--GACTTGTAATGAAA
ATACATTACAGTATTAAATTACAAATGAACATGCAAAATRAAAGGACTTGTAATRAAT

GCATTGTGAAGTCAA---ACCGAGTCTCTG--TGGATCTCAAAGCAAACTCTTAACTTAA
GCATTATGAAGTGATGATACTGATTTAATTAAATGGATCTCAAACAAAACCTTTAACTTAA

GGCACTTTGATTTTGCCAACAAATAATAACAAACATTAAGAGAAAAAATGATCCACTAC
GGCACTTTTATTTTGOCAACAAATAACAATAAACAA----ACATTGAAACGGTTCATAT

GAAATAACAAACGGCTAATGCACCTGAATTCT-CAGTAAAAAGACCTTCTCTCGCTAAC
AAAATAACAAATGGCTAATGTACCTGAATTTTTTCACTAAAAAAA--TGAAGTT-CTAAT

AGTTGCCAGCTGCCTCGTGTCTGTTTCCTACCAATGTCAAAACATGCGACACAGGGTGA
A---CCAGTTGCCTAGTGTCCACCTCCATCAATGTTACAAGCATGGCACTCAG---A

ATGGAGTCAACGGGAARGATTAAAGTTTGCGGTCTGTGTAAATCTCATGTACAAATATTC
ACAGAGACATGGAATAATTAAATCTGC-----AATCT--ATGTATAAATATTT

TGTGNCGTGGTTTATAAACATTTT-GATAAACCAGAAAAA
TGT---GGTTTATAAATTTTTTGTCTAAAACTACAGAAATAG

AAAA

(rat_cDNA: SEQ ID NO:7)
(human_5+3 corrected: SEQ ID NO:8)
(mus cDNA_5: SEQ ID NO:9)

[illegible]

rat
human_5+3_corrected
mouse_5_corrected

MQVRGREVSGLLISLTAVCLVVT PGSRACPRRCACYPTVEHVCTFRYLTSIPDGIPANVE
MKVKGRGITCLLVSVFAVICLVATPGGKACPRRCACYMTEVHCTFRYLTSIPDSIPPNVE
MQKRGREVSCLLISLTATCLVVT PGSRVCFRRACAYPTEVHCTFRDLTSIPD-GPANVE

rat
human_5+3_corrected
mouse_5_corrected

RINLGYNLSRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGQLSLOVLKMSYNKVQII
RINLGYNLSVRLMETDFSGLTLELLMLHSNGIHTIPDKTFSDLOALQVLKMSYNKVRKL
RVNLGYNSLRILTENDFSGLSRKLELLMLHSNGIHRVSDKTFSGQLSLOVLKMSYNKVQII

rat
human_5+3_corrected
mouse_5_corrected

RKDTFYGLGSVLRILHDENNIEFINPEAFYGLTSLRLVHLEGNRILT KLHPDTFVSLSYLQ
QKDTFYGLRSRLTRLEMDENNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYLQ
EKDTLYGLRSRLTRLEMDENNIEFINPEAFYGLTLRLVHLEGNRILT KLHPDTFVSLSYLQ

rat
human_5+3_corrected
mouse_5_corrected

IFKTSFIKYLELSDNF LTSLPKEMVSYMPNLESYLHGNEFTWCDCHLKWLSEWMOGNPDI
IFKISFIKFLYLSDNFLTSLSPKENVSYMPDLDSL YLHGNEFTWCDCHLKWLSDWIQ--PDV
IFKTSFIKXLYLDNF-TSLPKENVSSMPNLESYLHGNEFTWCDCHLKWLSEWMGNP---

rat
human_5+3_corrected
mouse_5_corrected

IKCKKDRSSSSPOQCPLCMNPRI SKGRPFAMVP SGAF LCTKPTIDPSLKS KSLVTOEDNG
IKCKKDRSPSSAQOQCPLCMNPRT SKGKPLAMVSAARAFCAKPTIDS GLKS KSLTILEDSS

rat
human_5+3_corrected
mouse_5_corrected

SASTSPQDFIEPFGSLSLNM TXXSGNKADMVCSIQKPSRTSPTA TEENDYIMINASFSST
SAFISPOGFMAFPFGLTI NM TDQSGNEARMVC SIQKPSRTSPIA TEENDYIVLNTSFSST

rat
human_5+3_corrected
mouse_5_corrected

NLVCSDVDNYHIQPWWQLALY8DSPLILERKPQTETPSLSRYKQVALRPEDI FT SIEA
FLVCNIDYGHIQPWWQLALY8DSPLILERSHLSETPOLYKYKQVAPKPEDIFTNIEA

rat
human_5+3_corrected
mouse_5_corrected

DVRADPFWFQQEKIVLQINRTATT TLSTLQIQFSTDAQIAL PRAENRAERLKWTMI LMNN
DIRADPSWLNQDQISLQINRTATT FSTLQIQYSSDAQITLPRAENRFVKHWMTI SRDNN

rat
human_5+3_corrected
mouse_5_corrected

PRLERTVLVGSTIALSCPGKGDP SPHEWLLADGSKVRAPYVSEDGRILL DKNGKLELM
TKLEHTVLVGGT VGLNCPGQGDP THVWLLADGSKVRAPYVSEDGRILL DKS GKELELM

rat
human_5+3_corrected
mouse_5_corrected

ADSFDAGLYHCISTNDADADVLTIRITVVEPYGESTHDSGVQH TVTGETL DLPC LSTGV
ADSFDGVYHCISSNYDDADILTYRITVVEPLVEAYQENG IHHTVFGETL DLPC HSTGI

rat
human_5+3_corrected
mouse_5_corrected

P DASISWILPGNVTFSPQRSRDQITLNGT LRILQVTFKDQGHYQCVAA NPBGADFSSFKV
PDASISWVIPGNVLYQSSRDKKVLNNGT LRILQVTFKDQGYTRCVAANPSGVDFLI PQV

rat
human_5+3_corrected
mouse_5_corrected

SVQKKQRNV EHDREAGSG LGEPNS8VSLKQ PASLKL SASALTG SEAGQVSGVHRKNK
SVKMGQRPLEHDGETE GSGLEDENPIAH LKEPPGAQLRTSALMEAEVGH TSSTSKRMN

rat
human_5+3_corrected
mouse_5_corrected

HRDLIHRRRGDSTLR RFREHRRQLPSARRIDPQRWAALLEKAKKN SVPKQENTTVKPV
YRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQRWAALLEKAKKNAMPDKRENTTVSFP

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rat      WPEHKYQLKSY6ETIEKGRPAVSMSPHLSLPEASTHASHWNTQKHAESVFDKKPGQN
human_5+3_corrected WAELYQFWHKPYSDLAERKGGKPEVSMATTGLSEATTIVSDWDGQKNTKKSDFDKKPVQEA
mouse_5_corrected  -----

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[illegible]

rat -TSKHLPYVSLPKTLKPKRIIGGKAASFVTPANSDFVLPCEAVGDLPIIHWTRVSSGX
human_5+3_corrected TTSKLLPFDLSRYIFEKPRIVGGKAASFVTPANSDFVLPCEAVGNPLTIHWTRVS-GL
mouse_5_corrected -----

rat EISQGTQKSRPHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFVLSVVFFPARILD
human_5+3_corrected DLSRGNQNSRVQVLPNGTLSIQRVSIQDRGQYLCASNLFGTDHLHVTLVVSYPPRIIE
mouse_5_corrected -----

rat RHVKEITVHFGSTVELKCRVEGMPRTVSWILANQTVVSETAKGSRKVVVTPDGTLLIYN
human_5+3_corrected RRTKEITVHSGSTVELKCRAEGRPSPTVWILANQTVVSESQGSRAVVTVDGTLVLHN
mouse_5_corrected -----

rat LSLYDRGFYKCVASNPGGQDSLVLVKIQVITAPPVILEQKROAIVGVLGSSKLPLCTAKGT
human_5+3_corrected LSIYDRGFYKCVASNPGGQDSLVLVKIQVIAAPPVILEQRRQVIVGTWGESKLPLCTAKGT
mouse_5_corrected -----

rat PQPSVHWVLYDGTTELKPLQLTHSRFFLYPMGTLYIRSIAPSVRGTTCIATSSSGSERRV
human_5+3_corrected PQPSVYVVLSDGTEVKELQFTNSKLFLFSNGTLYIRNLASSIRGTTECIATSSSGSERRV
mouse_5_corrected -----

rat VILTVEGETIPRIETASQKTEVNLGEKLLNCSATGDPKPRIIWRLPKKAVIDQWHRM
human_5+3_corrected VMLTMEERVTSPIEAASQKRTVNFQDALLNCSATGEPKPQIMWRLPKKAVIDQ----
mouse_5_corrected -----

rat GSRHIVYPNGSLVVGSVTEKDGAYLVCVARNKMGDDLILMHVRLRLTPAKIEQKQYFRKQ
human_5+3_corrected GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLILMHVSLRLKPAKIDKQYFRKQ
mouse_5_corrected -----

rat VLEGKDFQVDCRAGSGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGLTYFNNV
human_5+3_corrected VLEGKDFQVDCRAGSGSPVPEISWSLPGDTNINNAMQADDSGHRTRRYTLFNNGLTYFNKY
mouse_5_corrected -----

rat GMAEEGDYTCQAQNTLKGDKMKVHLTVLTAIPRIQSYKTMRLRAGETAVIDLCEVTGEP
human_5+3_corrected GVAEEGDYTCQAQNTLKGDKMKVHLTVITAAPRIQSNKTKRKIRAGDTAVLDCEVTGDP
mouse_5_corrected -----

rat KPNVFWLLPSNNVISFSNDRFTFAKRTLSTHKVKPLDSGDYVCVAQNPSGDDTKYKLD
human_5+3_corrected KPRLFNLLPSNDMISFSIDRYTFHANGSLTINKVKLLOSGEYVCVARNPSGDDTKMYKLD
mouse_5_corrected -----

rat IVSKPPLINGLYANKTVIKATAIPHSKKYFDCRADGIPSSQVWIMPNGNIFLPAPYFGSR
human_5+3_corrected VVSKPPLINGLYTNRTVIKATAVHRSHKHFDCAEGTSPSEVWIMPONIFLTAPYFGSR
mouse_5_corrected -----

rat VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGE5VLVVQLEVLMLRRPTFRNPFNEKIVA
human_5+3_corrected ITVHKNGTLEIRNVRLSDSADFTCVARNEGGESVLVVQLEVLMLRRPTFRNPFNEKIVA
mouse_5_corrected -----

rat QAGKPVALNCSVDGNPPPEITWLLPDGTQFANRPFNSPYLMAGNGSLILYKATRNK9GKY
human_5+3_corrected QLGKSTALNCSVDGNPPPEIIWLLPNGTRFSNGPQSYQYLIASNGSFIISKTTREDAGKY
mouse_5_corrected -----

rat RCAARNKVGYTEKLILLEIGQKPVILTYEPGMVKSVSGEPLSLHCVSDGIPKPNVKTTP
human_5+3_corrected RCAARNKVGYTEKLVILEIGQKPVILTYAPGTVKSIGESLSLHCVSDGIEKPNIKWIMP
mouse_5_corrected -----

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      rat      GGHVIDRPQVDGKYILHNGTLVLIKATTAHDQGNYYICRAQNSVGQAVIEVSVMVVAITRK
human_5+3_corrected  SGYVVDRPQINGKYILHNGTLVLIKATAYDRGNYYICRAQNSVGETLITVPVMIVAYPPR
mouse_5_corrected  -----

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rat      IINYLFRNMLRRTGEANQLHCVALGIPKPKVTWETPRESILSKATARKPFRSEMLHPQGT
human_5+3_corrected ITNRPPRSIVTRTGAAPQLHCVALGVFKPEITWEMPDHSLSTASKERTHGSEQLHIQGT
mouse_5_corrected  -----

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rat          LVIONLQTSDSGVYKCAQNLLGTDYATTYIQV
human_5+3_corrected LVIONPQTSDSGIYKCTAKNPLGSDYAATYIQV
mouse_5_corrected -----

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(rat: SEQ ID NO:10)
(human_5+3_corrected: SEQ ID NO:11)
(mouse_5_corrected: SEQ ID NO:12)

06-07-98

[illegible]

[illegible]

rat
 human_5+3_corrected
 SRIHVYPNGSLVVGSVTERKAGDYLCVARNKNGDOLVIMHVRLRLTPAKIBQKQYFKKQV
 SWIHVYPNGSLFIGSVTERKDSGYLCVARNKNGDOLIMHVSLRLPKAKIDHKQYFRKQV
 * *****,*:*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 LHGKDFQVDCASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFENGTLYPNNVG
 LHGKDFQVDCASGSPVPEISWSLDPGTMNNAMQADDSGHRTRRTLFNNGTLYPNNVG
 *****,*:*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 MAEGDYICSAQNTLGKDEKRVHLTVLTAIPRIQSYKTMLRAGETAVIDCEVTGEPK
 VAEEDYTCAQNTLGKDEKRVHLTVITAAPRIQSNKTKRIKAGDTAVLDCEVTGDEK
 ;***** * *****,*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 PNVFWLLPSMNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTYKLDI
 PKIFWLLPSNDMISFSDRYTFHANGSLINKVLLDSGEYVCVARNPSGDDTKTYKLDV
 ::*:*:*:*:*:*:*:*:*;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 VSKPPLINGLYANKTVIKATAIRHSKKYFDCRADGIPSSQVTWIMPNIPLPAPYFGSRV
 VSKPPLINGLYTNRTVIKATAVRHSKKHEDCRAEGTPSPVEMWINEPNIPLTAPYFGSRI
 *****,*:*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 TVHPNGTLEMNRILSDSADFTCVVRSEGGESVLVVQLEVLMLRPTFPNPFNEKIVAQ
 TVHKNGTLEIRNVRLSDSADFTCVARNEGGESVLVVQLEVLMLRPTFPNPFNEKIVAQ
 *** *****,*:*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 AGKPVALNCSVDGNPPPEITWILPDGTQFANRPHNSFYLMAGNGSLILYKATRNKSGKYR
 LGKSTALNCSVDGNPPPEITWILPDGTQFANRPHNSFYLMAGNGSLILYKATRNKSGKYR
 ,*:*:*:*:*:*:*:*:*;* ***,*****:**** **,*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 CAARNKVGYIEKLILLEIGQKPVILTYEPMVKSVSCEPLSLHCVSDGIPKPNVKTTPG
 CAARNKVGYIEKLIVILEIGQKPVILTYAPGTVKGISGESLSLHCVSDGIPKPNVKTTPG
 *****,*:*****;* *****,*****:**** **,*:*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 GHVIDRPQVDGKYILHENGTLVIKATTAHQGNVICRAQNSVGQAVISVSMVVAIPPRI
 GVVVDRPQINGKYILHDNGTLVIKATTAHQGNVICRAQNSVGHTLITVPMVVAIPPRI
 ,:*:*:*:*:*:*:*:*;* *****,*****:**** **,*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 INYLPNNMLRRTGEAMQLHCVLGIKPKVTVETPRHSLLSKATARKPHRSEMHPQGTIL
 TNPPPSIVTRTGAAQQLHCVLGVKPEITWEMPDSHLLSTASKERTHGSEQLHLQGTIL
 * **,*: **** *;* *****,*****:**** **,*:*:*:*:*:*:*:*:*

rat
 human_5+3_corrected
 VIONLQTSDSGVYKCAQNLLGTDYATYIOVL
 VIONPQTSDSGIYKCTARNPLGSDYATYIOVI
 **** *:*:*:*:*;* *****,*****:**** **,*:*:*:*:*:*:*:*

(rat: SEQ ID NO:13)

(human_5+3_corrected: SEQ ID NO:14)

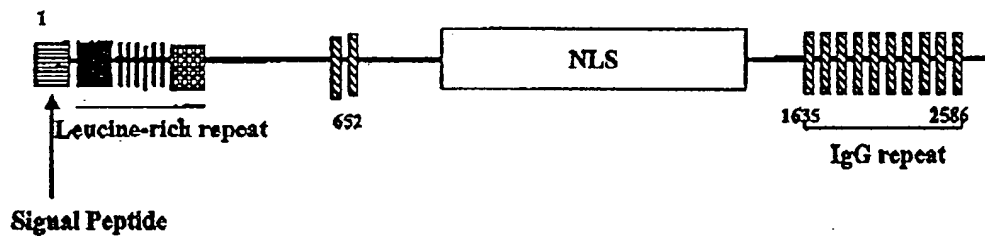
MQKRGREVSCLLISLTAICLVVTPGSRVCPRRACAYVPTEVHCTFRDLTSIPDGPANVER
 VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQIE
 KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF
 KTSFIKXLYLYDNFTSLPKEMVSSMPNLESYLYHGNPWTCDCHLKWLSEWMQGNP
 (SEQ ID NO: 15)

MKVKGRGITCLLVSFVAVICLVATPGGKACPRRCACYPMPTEVHCTFRYLTSIPDSIPPNEVE
RINLGYNLSVRLMETDFSGLTKELELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK
LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDFTFVLSLSYL
QIFKISFIKFLYLSDNFLTSLPQEMSYMPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
AFISPPQGFMAPFGSLTLNMTDQSGNEANMVCISIQKPSRTSPIAFTEENDYIVLNTSFSTFL
VCNIDYGHQIPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR
ADPSWLMQDQISLQLNRTATTFTSLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNNTK
LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
ADSFDTG VYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLIDLPCSTGIP
DASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYRCAVAAANPSGVDFLIFQV
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVKGHTSSTSKRH
NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALEKAKKNAMPDKRENTTV
SPPPVVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
YGTEFSPV VNSQILPPEEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG
ATEFQDSDQMGRGREHFQSRPPITVRTMIKD VNVKMLSSTTNKLLLESVNSHQTSVREV
SEPRHNHFYSHTTQILSTSTFPSPDHTAAHSQFPPIRNSTVNIPLFRRFGRQRKIGGRGRIIS
PYRTPVLRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRELTTATAALSFPSAAPI
TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
SIPMEKTHKVNASYPRVSSSTNEAKRDSVITSSLSGAIKPPMTIATFRSRRKIPWQQNFV
NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRLSTSVMQIPSNTLTT
AHHTTTKTHNPGSLPTKKELFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE
TQTERSRAQTIQREQEPQKKNRTPDNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
ISFHSRTLNLTDVIEELAQASTQTLKSTIASSETLSSKSHQSTTTRKASLDTPIPPFLSSSAT
LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLMQMPSSQLEPLTSSTSNLL
HSTPMPALTTVKSQNSKLTSPSWAEQFWHKPYSDIAEKGGKPEVSMMLATTGLSEATTLV
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[illegible]

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 NO: 16)

Figure 19



000543 043302
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Figure 20

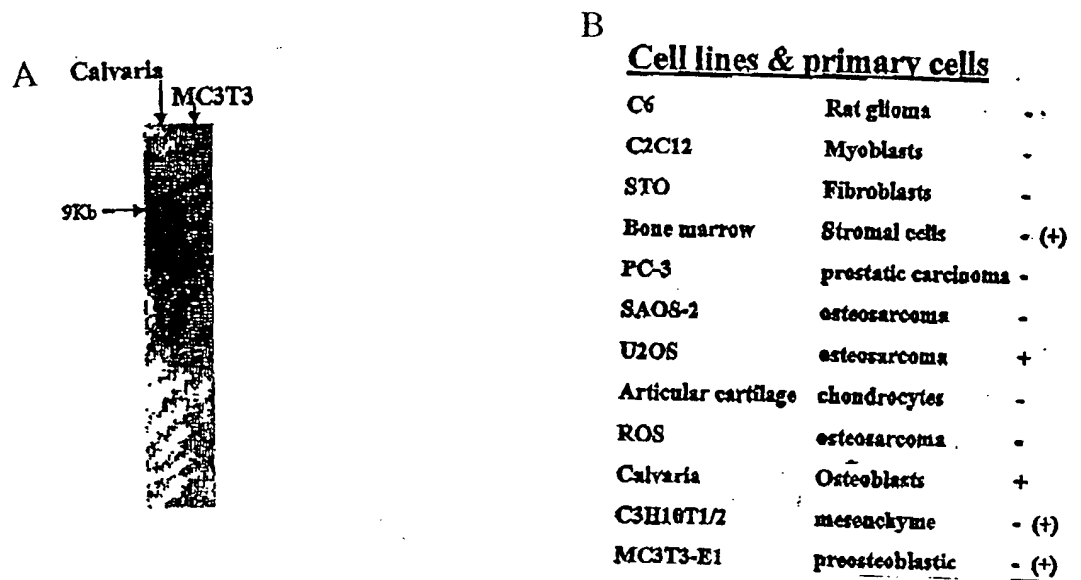
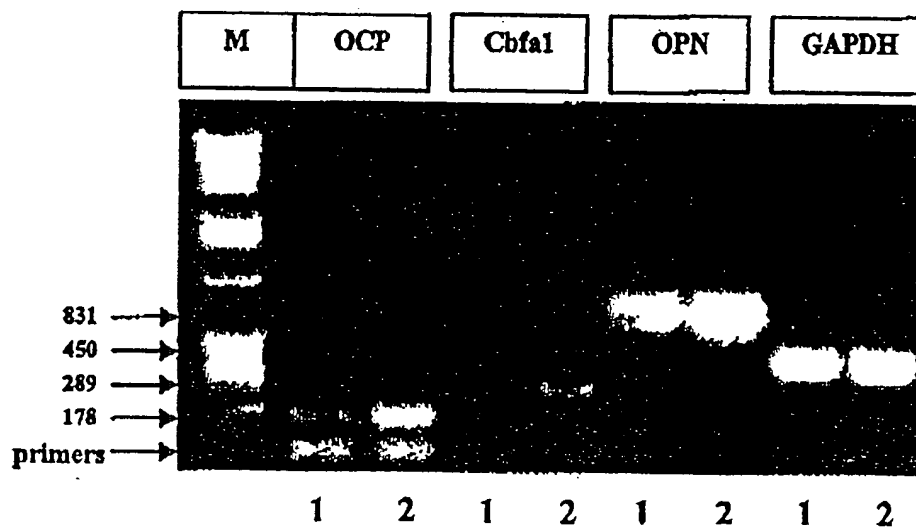


Figure 21



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Figure 22

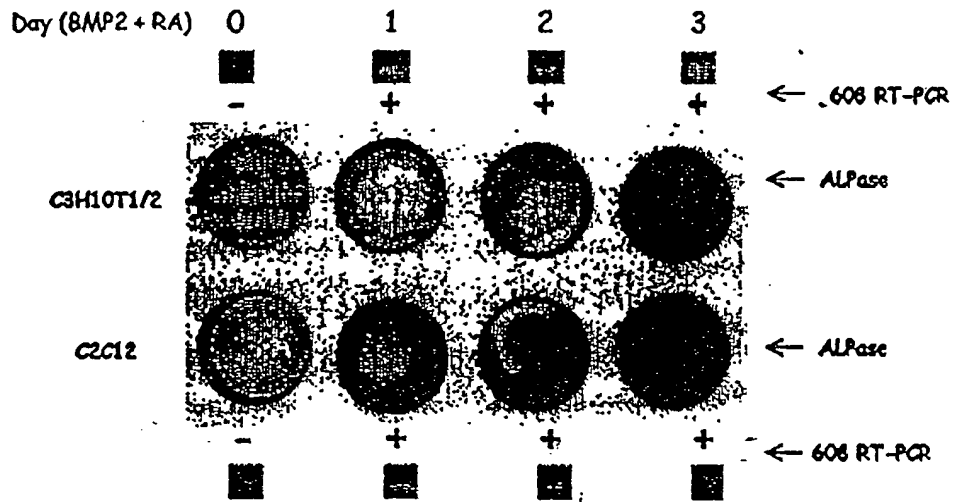
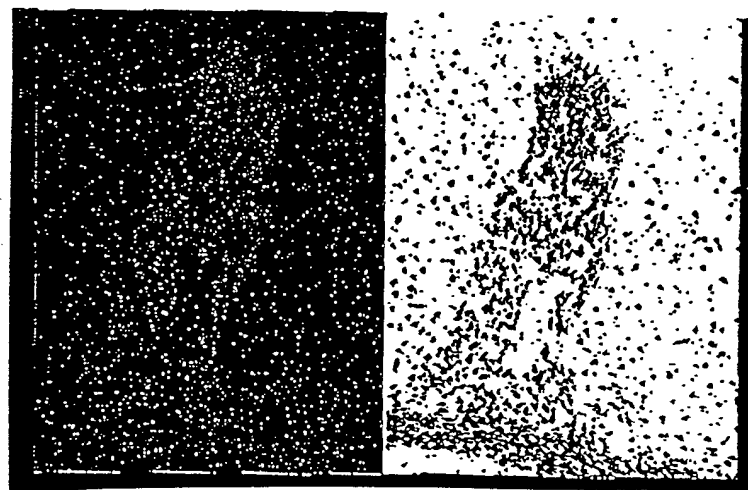


Figure 23



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Figure 24

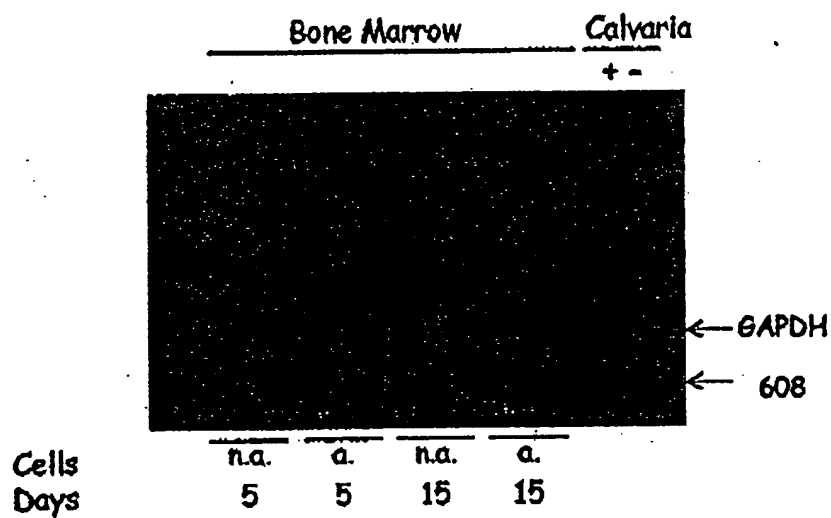
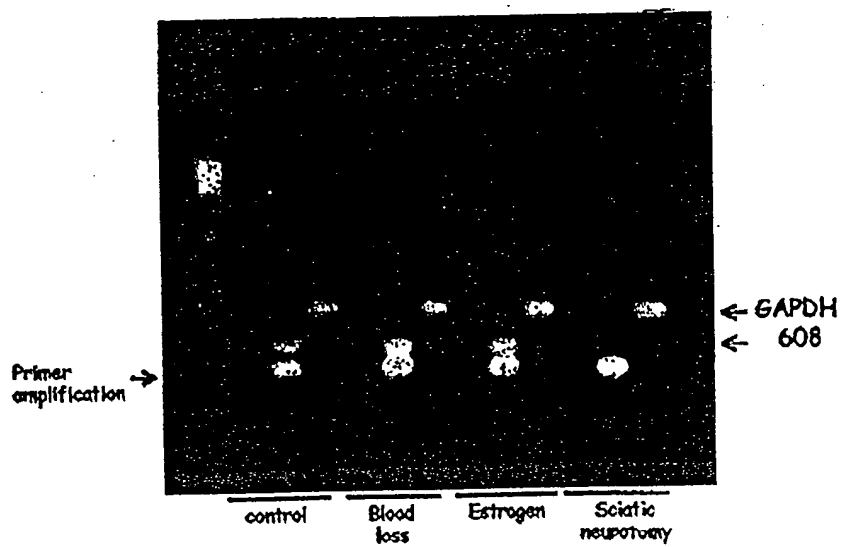


Figure 25



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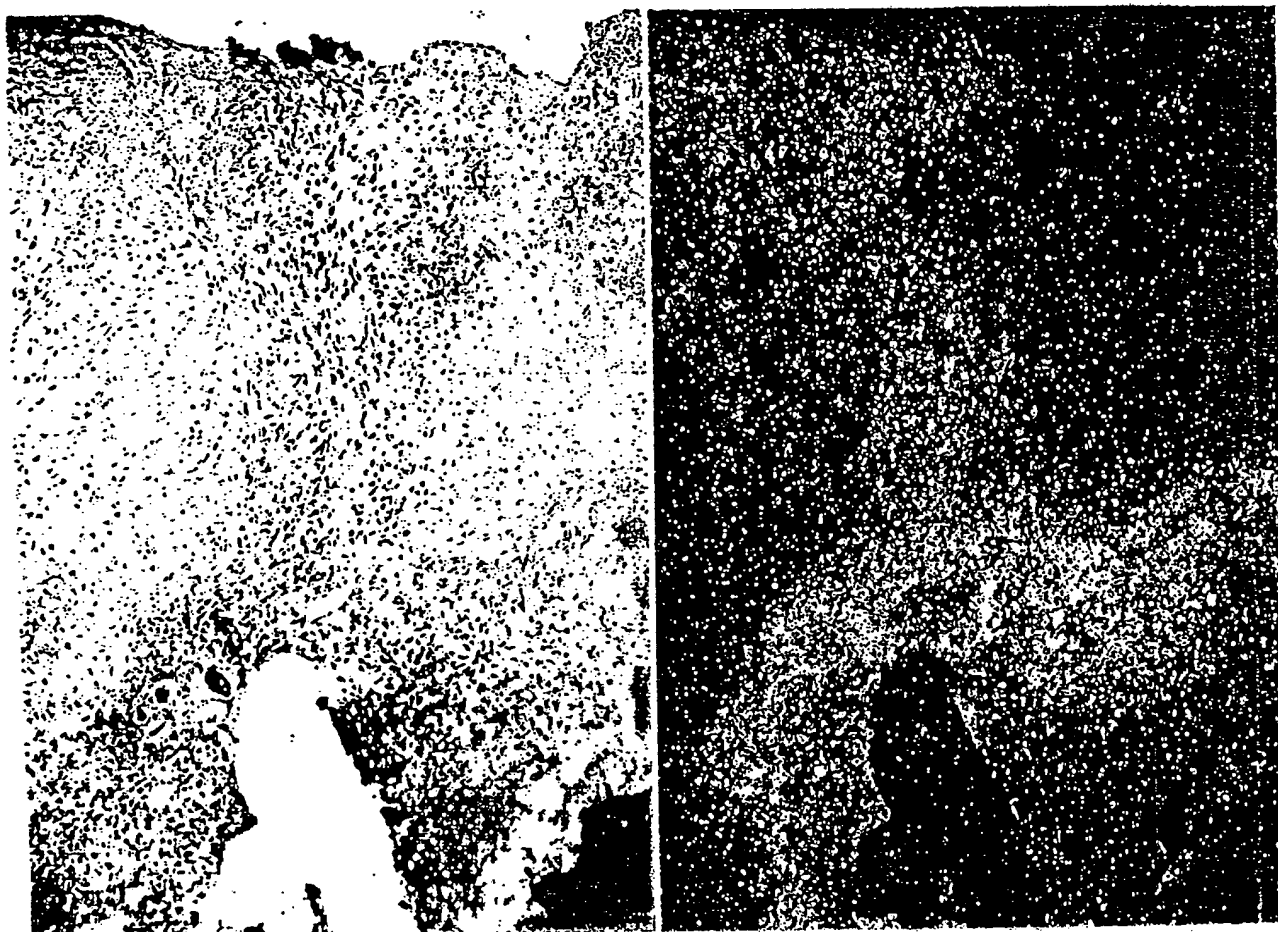
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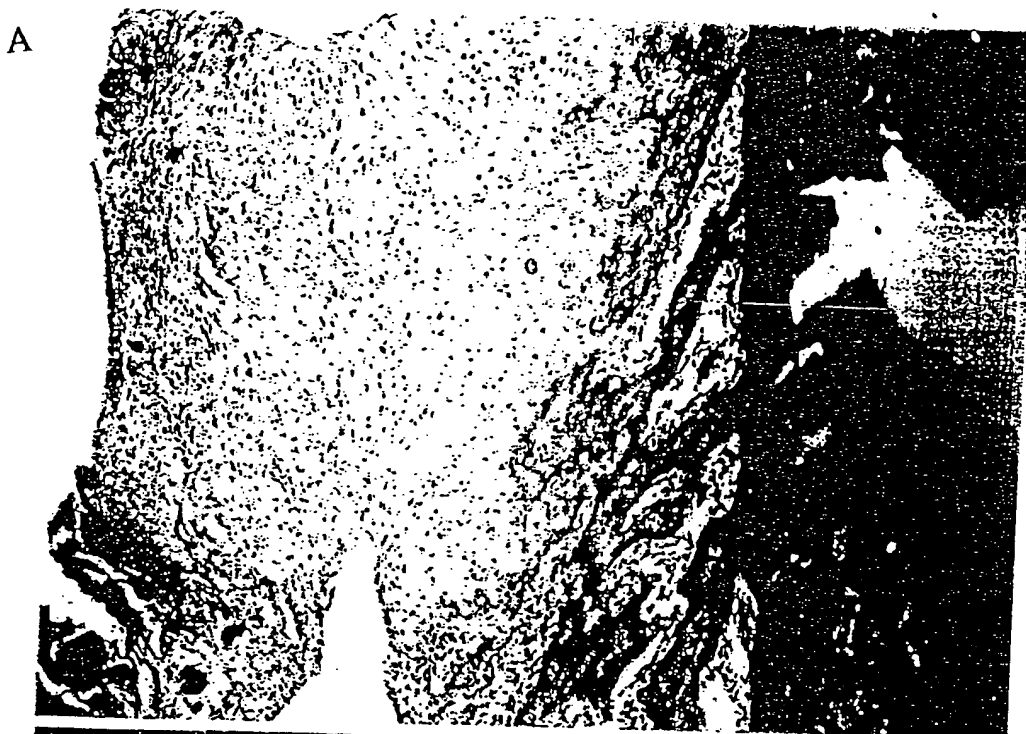


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Figure 27

B

[illegible]

[illegible]

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Figure 29

A



B



00005129.012202

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Figure 30



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Figure 31



00005430.042002

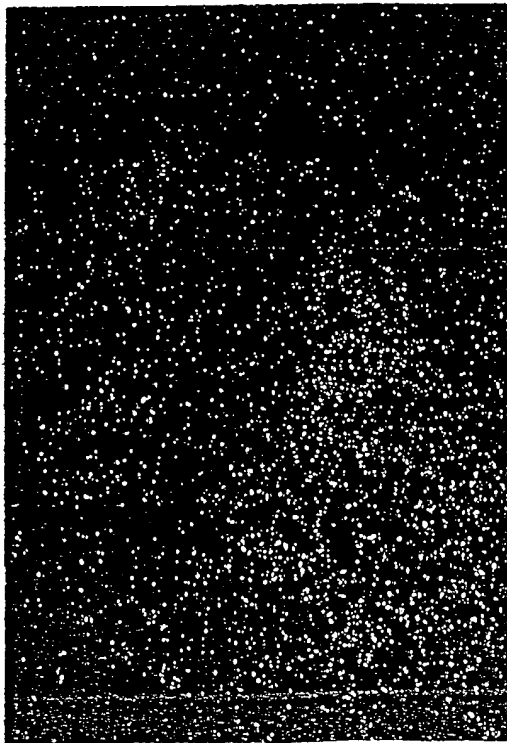
59/90

Figure 32

A



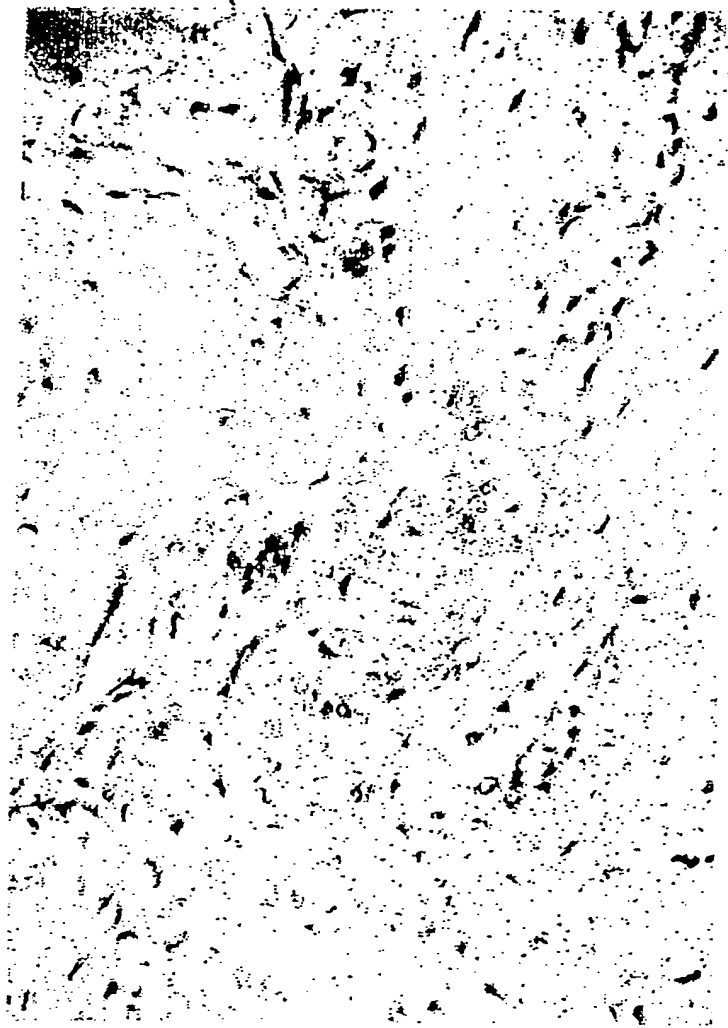
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60/90

Figure 33



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Figure 34

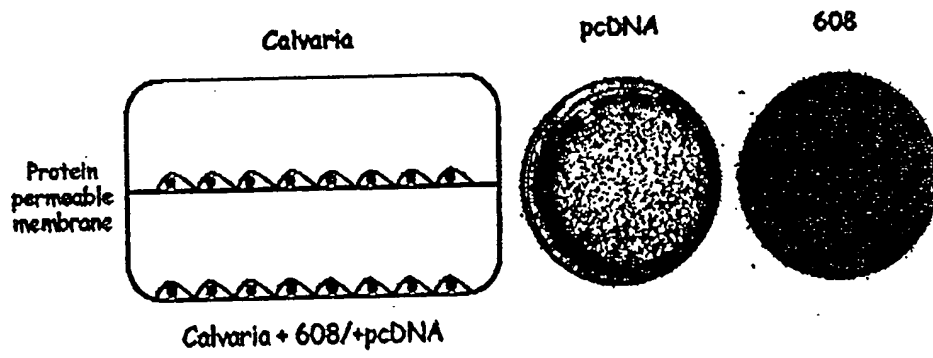
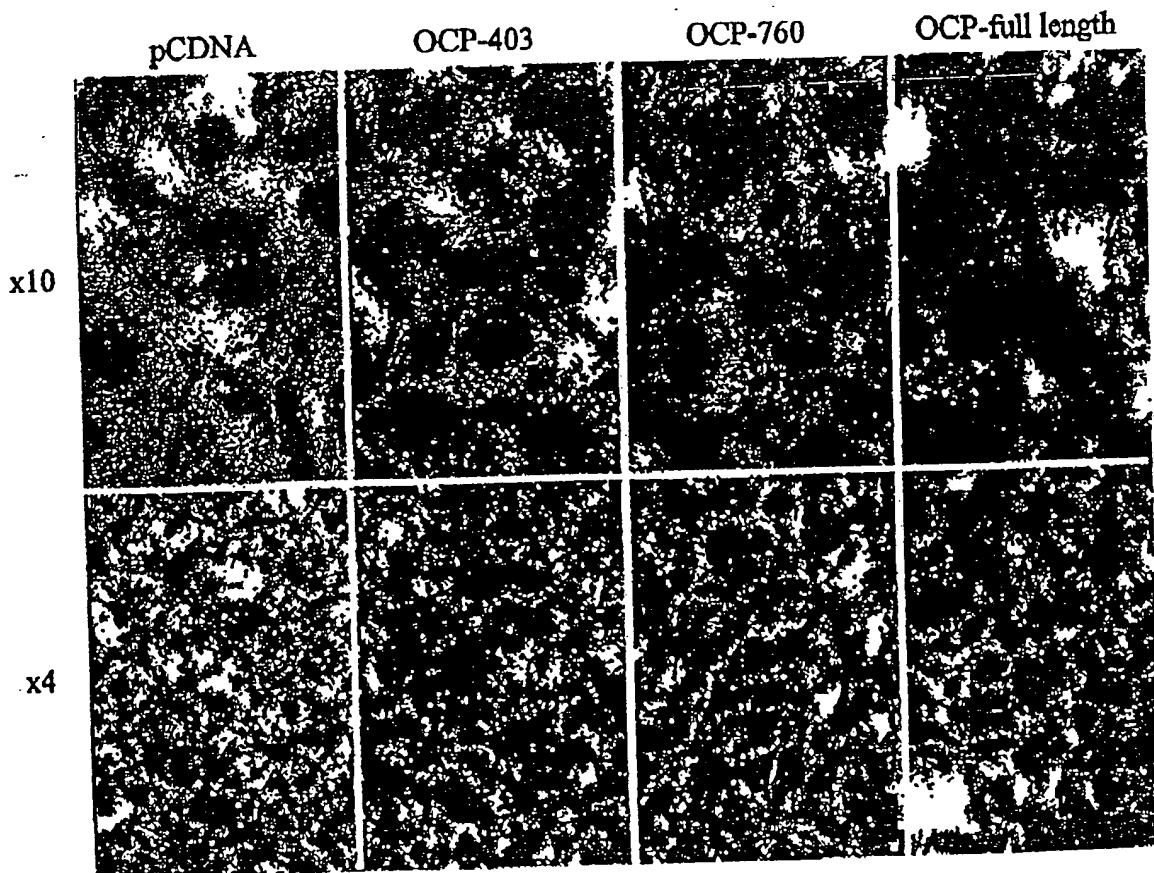


Figure 35



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Figure 36

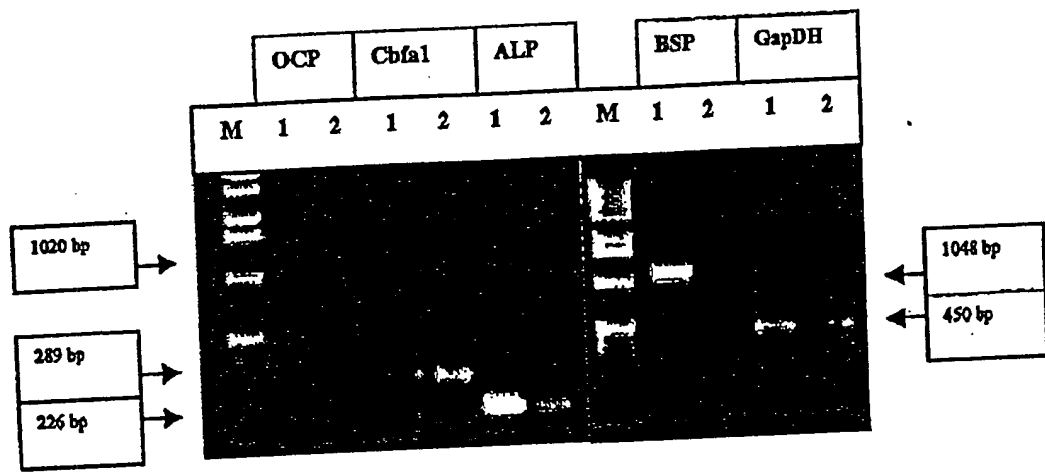


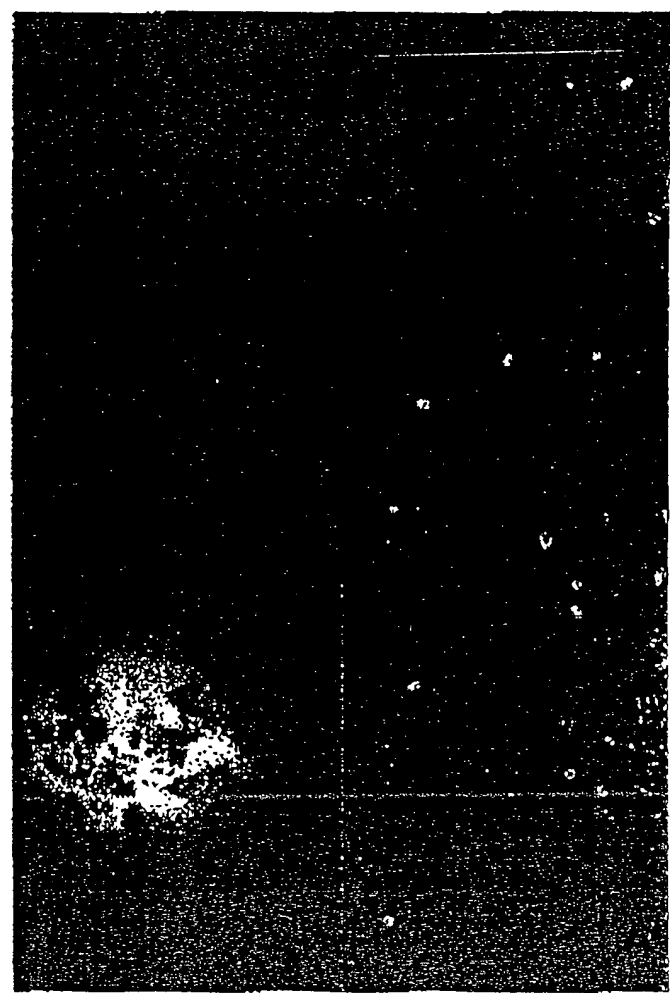
Figure 37

x 4

x 10

pCDNA
ROS stable line

OCP
ROS stable line



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Figure 38

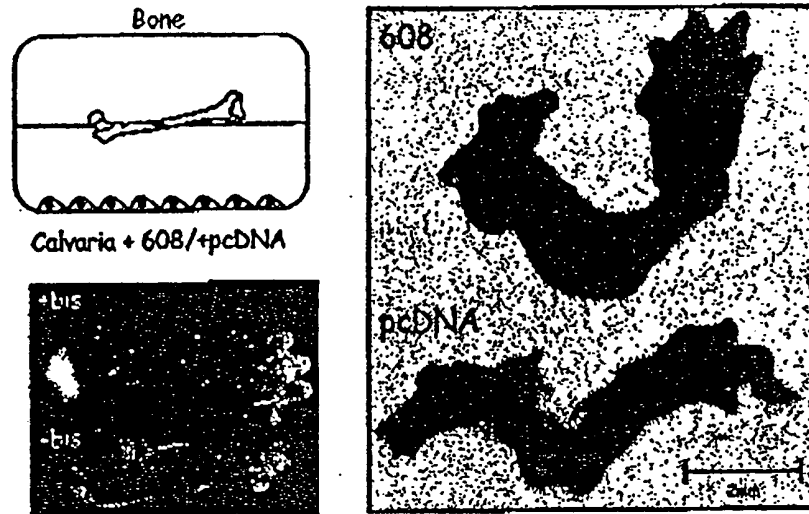
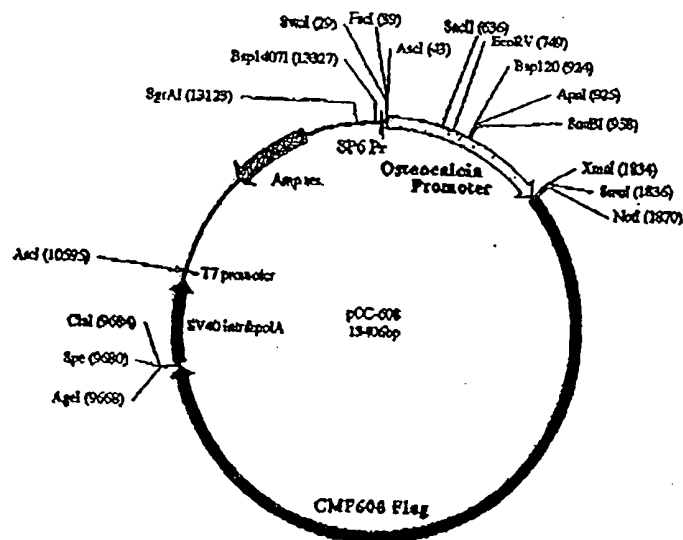
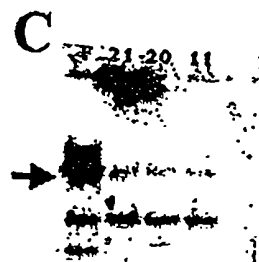
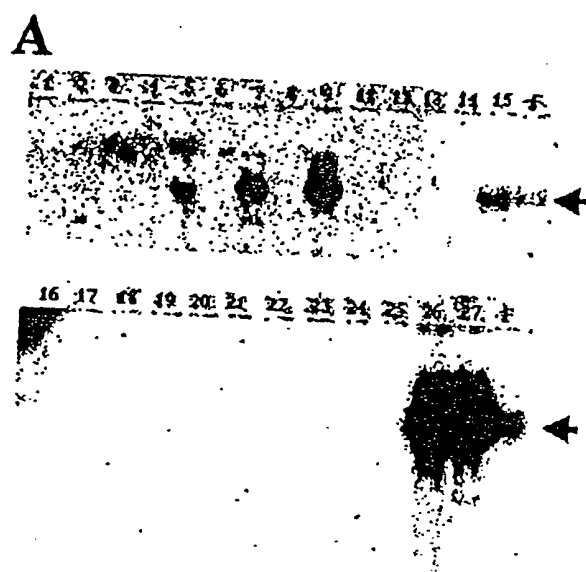


Figure 39



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Figure 40



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Figure 41

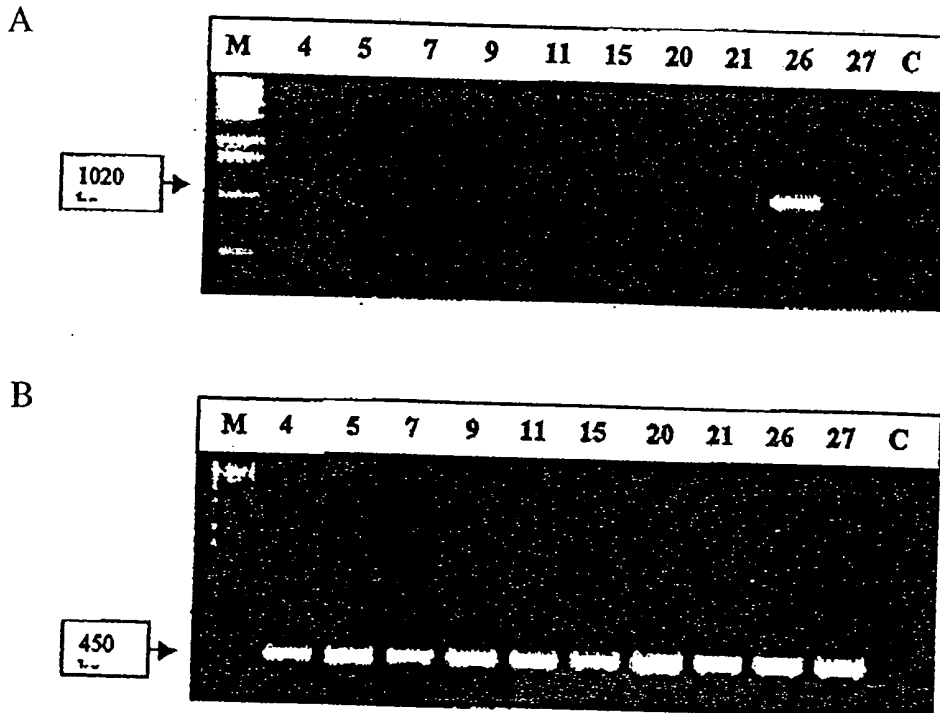
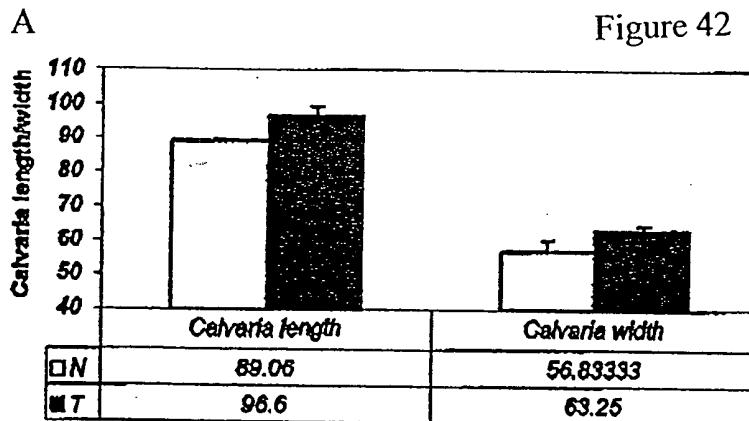
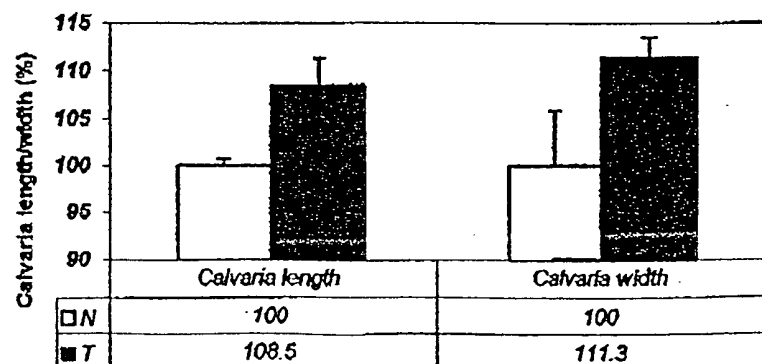


Figure 42



B



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Figure 43

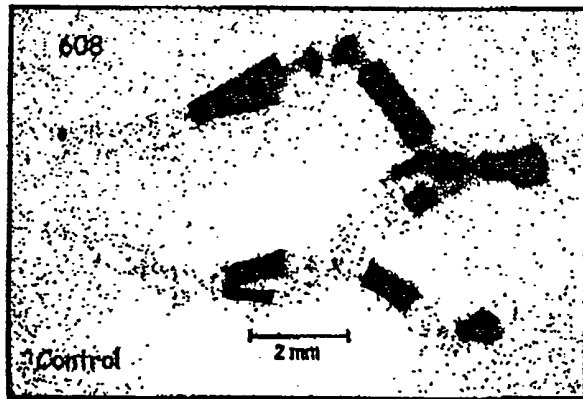
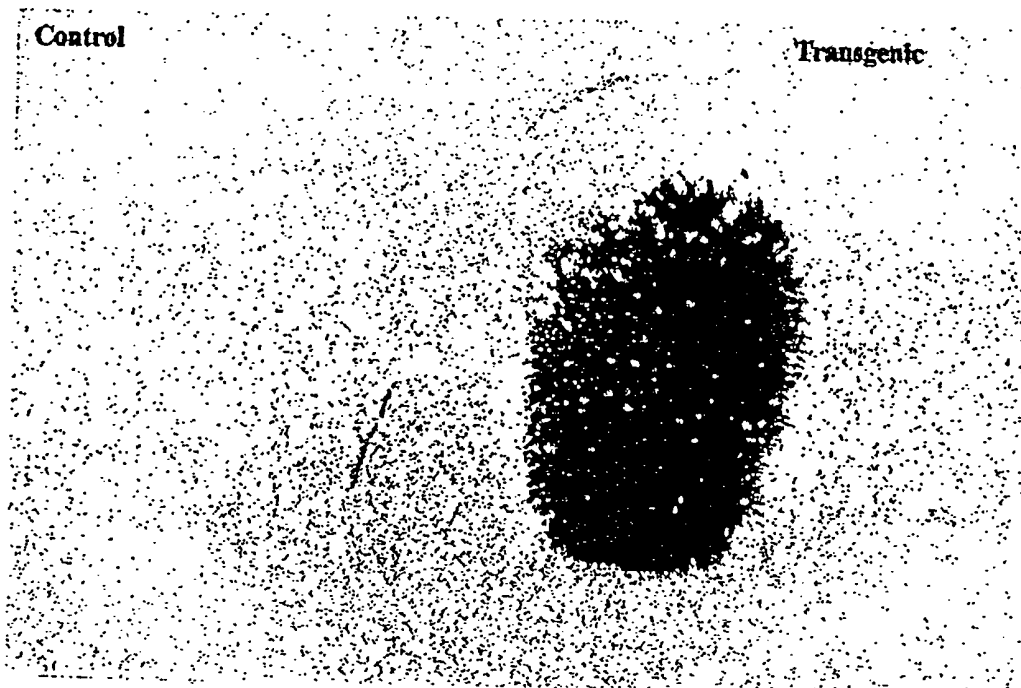


Figure 44



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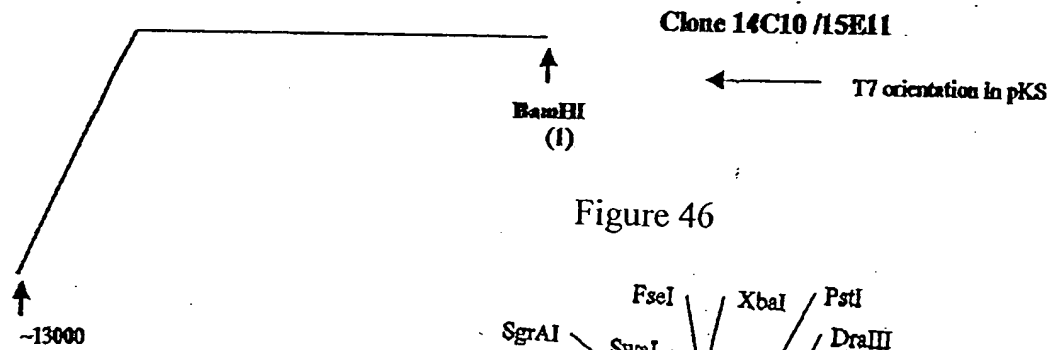
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Figure 46

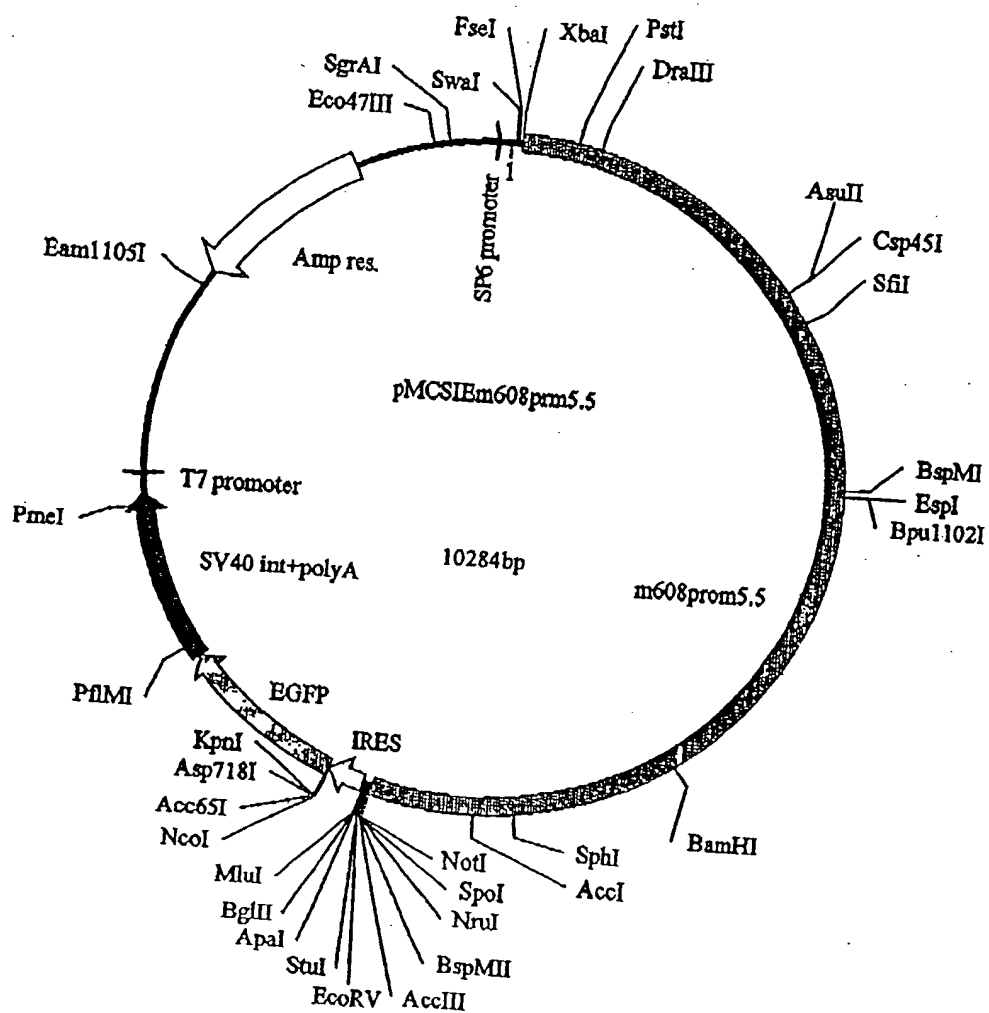


Figure 47

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Exon1

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NotI site

(SEQ ID NO:17)

00005429 : 042203

Figure 48

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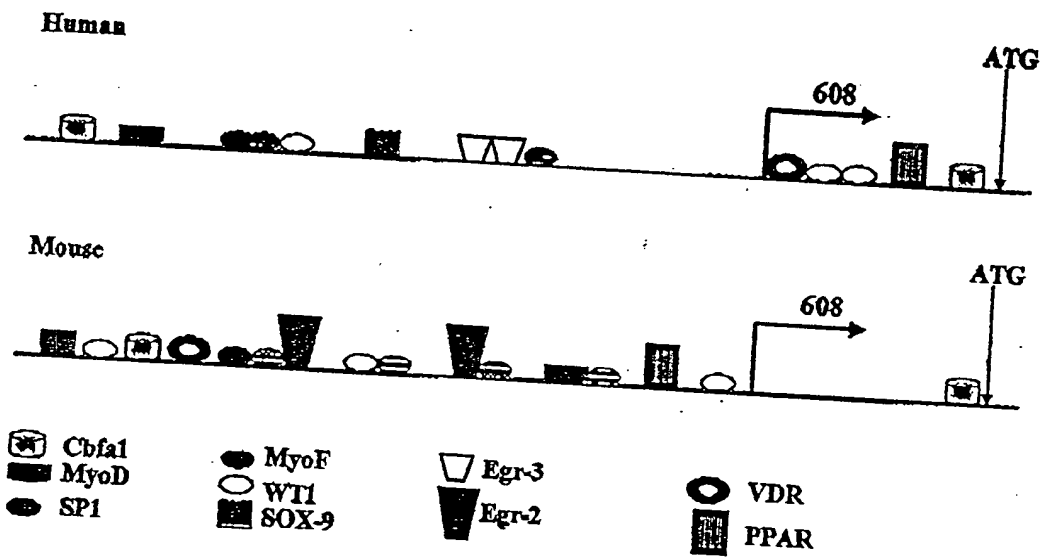
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(SEQ ID NO:18)

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Figure 49



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[illegible]

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[illegible]

Figure 52

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[illegible]

[illegible]

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GGTTCGTGAG GCCTCGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG
AGACGGAGTA CGGCCCTTCG GTCACCAGCA TCCCCGTGAT TGTGATCGCC
TATCCTCCCC GGATCACCAG CGAGCCCACC CCGGTCATCT ACACCCGGCC
CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT CCCAAAGCTG
ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTGAG
GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCAGGGAT CACTGACCAT
CCAGCATGCC ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA
ACATTCTCGG CAGTGACTCC AAAACAACCT ACATCCACGT CTTCTGAAAT
GTGGATTCCA GAATGATTGC TTAGGAACTG ACAACAAAGC GGGGTTTGTA
AGGGAAGCCA GGTGGGGGAA TAGGAGCTCT TAAATAATGT GTCACAGTGC
ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT
GAGACACTTT CTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAGGGTG
TCTGTGCTCT GACTGCAATT TTTCTTCTTT TGCAAATGCC ACTCGACTGC
CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCATCA AAAATAAGCC
ATAGACATGA ACAACACCTC ACTACCCCAT TGAGAGACGCA TCACCTAGTT
AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCCAGAT TGACAAGTCA
TCTTTCAGTT ATTCCTCTG TCACTTCAAA ACTCCAGCTT GCCCAATAAG
GATTTAGAAC CAGAGTGACT GATATATATA TATATATTTT AATTCAGAGT
TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTTCTTCC
TGGAATCAC TTTTATATA ATGTTTTATA TATATATTTT TTCCTTCAA
ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT ATTAATAA
ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA
ATATAATTTT AAAAAATTTT TCTCCAACCT CTTCAAATT CAGTCACCAC
TGTTATATTA CTTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT
AGATTTCCTT GTATGCAAAG TTTTGTGTA AAGCTGTGCT CAGAGGAGGT
GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACTTTACAG AATTGAATCT
AGAGTCTTCC CCGAAAAGCC CAGAACTTC TCTGCAGTAT CTGGCTTGTC
CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC
CCATGAATAA TACACGACCT GTTATTTCCA TGACTGCTTT ACTGTATTTT
TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCCCAAAA AAAAA

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Human OCP: nucleotide sequence of ORF

ATGAAGGTA AAAAGGCAGAGGAATCACCTGCTTGCCTGGTCTCCTTTGCTGTGATCTGC
CTGGTCGCCACCCCTGGGGGCAAGGCCTGTCCTCGCCGCTGTGCCTGTTATATGCCT
ACGGAGGTACACTGCACATTTTCGGTACCTGACTTCCATCCCAGACAGCATCCCCGCC
AATGTGGAACGCATCAATTTAGGATACAACAGCTTGGTTAGATTGATGGAAACAGAT
TTTTCTGGCCTGACCAAACCTGGAGTTACTCATGCTTCACAGCAATGGCATTACACA
ATCCCTGACAAGACCTTCTCAGATTTGCAGGCCTTGACAGGTCTTAAAAATGAGCTAT
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CTGAACTGCCCAGGCCAAGGAGACCCACCCACACGTGGATTGGCTTCTAGCTGAT
GGAAGTAAAGTGAGAGCCCCCTTATGTCAGTGAGGATGGACGGATCCTAATAGACAAA
AGTGGA AAAATTGGA ACTCCAGATGGCTGATAGTTTTGACACAGGCGTATATCACTGT
ATAAGCAGCAATTATGATGATGCAGATATTCTCACCTATAGGATAACTGTGGTAGAA
CCTTTGGTCGAAGCCTATCAGGAAAATGGGATTCATCACACAGTTTTTCATTGGTGAA
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TTTTACAAATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCACTGCTGGTTAAATA
CAAGTCATTGCAGCACCACTGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGC
ACTTGGGGTGAAAGTTTAAACTGCCCTGTACTGCAAAAGGAACCTTCAGCCCAGC

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GTTTACTGGGTCCTCTCTGATGGCACTGAAGTGAAACCATTACAGTTTACCAATTCC
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 CCCAAACCCCAAATAATGTGGAGGTTACCATCCAAGGCTGTGGTCGACCAGTGGAGC
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 AGTGGTGTCTACTTGTGTGTGGCAAGAAACAAAATGGGGGATGATCTGATACTGATG
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 CAAGTGCTCCATGGGAAAGATTTCCAAGTAGATTGCAAAGCTTCCGGCTCCCCAGTG
 CCAGAGATATCTTGGAGTTTGCCTGATGGAACCATGATCAACAATGCAATGCAAGCC
 GATGACAGTGGCCACAGGACTAGGAGATATACCTTTTCAACAATGGAACCTTATAC
 TTCAACAAAGTTGGGGTAGCGGAGGAAGGAGATTATACTTGCTATGCCCAGAACACC
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 GGGGATGACACCAAAATGTACAACTGGATGTGGTCTCTAAACCTCCATTAATCAAT
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 TCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAACG
 TATATTCAAGTAATCTGA

Figure 54 Human OCP: predicted amino acid sequence

MKVKGRGITC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS
 IPDSIPPNVE RINLGYNSLV RLMETDFSGL TKLELLMLHS NGIHTIPDKT
 FSDLQALQVL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY
 GLNFLRLVHL EGNQLTKLHP DTFVLSYLQ IFKISFIKFL YLSDNFLTSL
 PQEMVSYMPD LDSLYLHGNP WTCDCCHKWL SDWIEKPDV IKCKKDRSPS
 SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS
 SAFISPQGM APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND
 YIVLNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL
 YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI
 QYSSDAQITL PRAEMRPVKH KWTMISRDNM TKLEHTVLVG GTVGLNCPGQ
 GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH
 CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI
 PDASISWVIP GNNVLYQSSR DKKVLNNGTL RILQVTPKDQ GYYRCVAANP
 SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT
 SALMEAEVGK HTSSTSKRHN YRELTQLRRG DSTHRRFREN RRHFPPSARR
 IDPQHWALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML
 ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYG T EFSPVVNSQI
 LPPEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA
 TEFQDSQMG RGREHFQSRP PITVRTMIKD VNVKMLSST NKLLLESVNT
 TNSHQTSVRE VSEPRHNHFY SHTTQILSTS TFPSPHTAA HSQFPPIRNS
 TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRSIFR STTRGSSEKS
 TTAFSATVLN VTCLSLPRE RLTTATAALS FPSAAPITFP KADIARVPSE
 ESTTLVQNPL LLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTISI
 PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR
 RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF
 HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMPLPS
 IISKDSSTKS IISTQTAIPA TTPTFPASVI TYETQTERS AQTIQREQEP
 QKKNRTDPNI SPDQSSGFTT PTAMTPPALA FTHSPPENTT GISSTISFHS
 RTLNLTDVIE ELAQASTQTL KSTIASSETTL SSKSHQSTTT RKASLDTPIP
 PFLSSSATLM PVPISPPFTQ RAVTDTRGDS HFRLMTNTVV KLHESSRHLN
 QMPSSQLEPL TSSTSNLLHS TPMPALTTVK SQNSKLTPSP WAHEYQFWHKP
 YSDIAEKGGK PEVSMLATTG LSEATTLVSD WDGQKNTKKS DFDKKPVQEA
 TTSKLLPFDS LSRYIFEKPR IVGGKAASFT IPANSDAFLP CEAVGNPLPT
 IHWTRVSGLD LSRGNQNSRV QVLPNGTSLI QRVEIQDRGQ YLCSASNLF
 TDHLHVTLSV VSYPPRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI
 LANQTVVSES SQGSRQAVVT VDGTLLVHLN SIYDRGFYKC VASNPGGQDS
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 MLTMEERVTS PRIEASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK
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 LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM
 QADDSGHRTR RYTLFNNGTL YFNKVGVAEE GDYTCYAQNT LGKDEMKVHL
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 FSIDRYTFHA NGSLTINKVK LLDSGEYVCV ARNPSGDDTK MYKLDVVSKP
 PLINGLYTNR TVIKATAVRH SKKHFDCAE GTPSPEVMWI MPDNIFLTAP
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 RRPTFRNPEN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ
 SYQYLIASNG SFIISKTTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPMI

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